GenCore version 4.5

OM nucleic - nucleic search, using sw model

Run on: September 18, 2002, 23:45:35 ; Search time 3921.26 Seconds
(without alignments)
11532.580 Million cell updates/sec

Title: US-09-695-451-1
Perfect score: 2161
Sequence: 1 cggcccagtgatcttgaacc.....tacactaaaattctgaagtt 2161

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1797656 seqs, 10463268293 residues

Total number of hits satisfying chosen parameters: 524256

Minimum DB seq length: 0
Maximum DB seq length: 30

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:*
1: gb_ba:*
2: gb_htg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vi:*
15: em_ba:*
16: em_fun:*
17: em_hum:*
18: em_in:*
19: em_mu:*
20: em_om:*
21: em_or:*
22: em_ov:*
23: em_pat:*
24: em_ph:*
25: em_pl:*
26: em_ro:*
27: em_sts:*
28: em_un:*
29: em_vi:*
30: em_htg_hum:*
31: em_htg_inv:*
32: em_htg_other:*
33: em_htgo_inv:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	28	1.3	28	6	AR090141	AR090141 Sequence
c 2	28	1.3	28	6	AR090142	AR090142 Sequence
3	27	1.2	27	6	A26401	A26401 cDNA fragme
4	24.8	1.1	28	6	A29671	A29671 Oligonucleo
5	24	1.1	24	6	AR096333	AR096333 Sequence
6	24	1.1	28	6	A63563	A63563 Sequence 4
c 7	23.8	1.1	29	6	A26411	A26411 oligonucleo
c 8	23	1.1	23	6	A39497	A39497 Sequence 1
9	23	1.1	23	6	AR096331	AR096331 Sequence
10	23	1.1	27	6	AR131318	AR131318 Sequence
11	23	1.1	27	6	AR134770	AR134770 Sequence
12	22.8	1.1	26	6	A29670	A29670 Oligonucleo
c 13	22.6	1.0	30	6	A43784	A43784 Sequence 9
14	22.6	1.0	30	6	A62991	A62991 Sequence 3
c 15	22.6	1.0	30	6	A62995	A62995 Sequence 7
16	22.6	1.0	30	6	AX104902	AX104902 Sequence
c 17	22.6	1.0	30	6	AX104903	AX104903 Sequence
c 18	22.6	1.0	30	6	AX351711	AX351711 Sequence
19	22.6	1.0	30	6	E04638	E04638 Synthesized
c 20	22.6	1.0	30	6	I84450	I84450 Sequence 9
c 21	22.2	1.0	29	6	AX052989	AX052989 Sequence
c 22	22	1.0	30	6	AR084541	AR084541 Sequence
c 23	22	1.0	30	6	AR165925	AR165925 Sequence
c 24	22	1.0	30	6	E34522	E34522 SCA7 gene a
c 25	22	1.0	30	6	I84405	I84405 Sequence 6
26	22	1.0	30	6	I84410	I84410 Sequence 11
c 27	21.8	1.0	25	6	I29929	I29929 Sequence 42
c 28	21.6	1.0	29	6	AR162080	AR162080 Sequence
c 29	21.6	1.0	29	6	AR166605	AR166605 Sequence
30	21.6	1.0	29	6	AX048408	AX048408 Sequence
c 31	21.6	1.0	29	6	AX048409	AX048409 Sequence
c 32	21.6	1.0	29	6	AX052994	AX052994 Sequence
c 33	21.6	1.0	29	6	AX353685	AX353685 Sequence
c 34	21.6	1.0	30	6	AR051244	AR051244 Sequence
c 35	21.6	1.0	30	6	AR127791	AR127791 Sequence
c 36	21.6	1.0	30	6	I28373	I28373 Sequence 12
c 37	21.4	1.0	23	6	AR089237	AR089237 Sequence
c 38	21.2	1.0	29	6	AX181697	AX181697 Sequence
39	21.2	1.0	30	6	I14296	I14296 Sequence 4
40	21	1.0	21	6	A19909	A19909 Synthetic 5
41	21	1.0	21	6	A19910	A19910 Synthetic 3
c 42	21	1.0	21	6	A19911	A19911 Synthetic 3
c 43	21	1.0	21	6	A19912	A19912 Synthetic 5
c 44	21	1.0	21	6	AR131319	AR131319 Sequence
c 45	21	1.0	21	6	AR134771	AR134771 Sequence

ALIGNMENTS

RESULT 1
AR090141
LOCUS AR090141 28 bp DNA linear PAT 07-SEP-2000
DEFINITION Sequence 261 from patent US 5994076.
ACCESSION AR090141
VERSION AR090141.1 GI:10016896
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 28)
AUTHORS Chenchik,A., Jokhadze,G. and Bibilashvilli,R.
TITLE Methods of assaying differential expression
JOURNAL Patent: US 5994076-A 261 30-NOV-1999;
FEATURES Location/Qualifiers
source 1. .28
/organism="unknown"
BASE COUNT 5 a 9 c 7 g 7 t
ORIGIN

Query Match 1.3%; Score 28; DB 6; Length 28;
Best Local Similarity 100.0%; Pred. No. 1.8e+05;

```
  Matches   28;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy   1645 tctaaggaccgtcctgcgagatcgcctt 1672
          ||||||||||||||||||||||||||||
Db      1 TCTAAGGACCGTCCTGCGAGATCGCCTT 28


RESULT
AR090142/c
LOCUS       AR090142                  28 bp    DNA     linear   PAT 07-SEP-2000
DEFINITION  Sequence 262 from patent US 5994076.
ACCESSION   AR090142
VERSION     AR090142.1  GI:10016897
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 28)
  AUTHORS   Chenchik,A., Jokhadze,G. and Bibilashvilli,R.
  TITLE     Methods of assaying differential expression
  JOURNAL   Patent: US 5994076-A 262 30-NOV-1999;
FEATURES             Location/Qualifiers
     source          1. .28
                     /organism="unknown"
BASE COUNT        8 a      8 c      8 g      4 t
ORIGIN


  Query Match             1.3%;  Score 28;  DB 6;  Length 28;
  Best Local Similarity   100.0%;  Pred. No. 1.8e+05;
  Matches   28;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy   1864 tgagggacgctatgcctcatgcccgttt 1891
          ||||||||||||||||||||||||||||
Db     28 TGAGGGACGCTATGCCTCATGCCCGTTT 1


RESULT   3
A26401
LOCUS       A26401                    27 bp    DNA     linear   PAT 25-APR-1995
DEFINITION  cDNA fragment from patent EP0417563.
ACCESSION   A26401
VERSION     A26401.1  GI:904957
KEYWORDS    .
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequence.
REFERENCE   1  (bases 1 to 27)
  AUTHORS   Brockhaus,M., Dembic,Z., Gentz,R., Lesslauer,W., Loetscher,H. and
            Schlaeger,E.J.
  TITLE     TNF-binding proteins
  JOURNAL   Patent: EP 0417563-A 12 20-MAR-1991;
            F. HOFFMANN-LA ROCHE AG
FEATURES             Location/Qualifiers
     source          1. .27
                     /organism="synthetic construct"
                     /db_xref="taxon:32630"
BASE COUNT        8 a      3 c     11 g      5 t
ORIGIN


  Query Match             1.2%;  Score 27;  DB 6;  Length 27;
  Best Local Similarity   100.0%;  Pred. No. 2.9e+05;
  Matches   27;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    364 agggagaagagagatagtgtgtgtccc 390
          |||||||||||||||||||||||||||
Db      1 AGGGAGAAGAGAGATAGTGTGTGTCCC 27


RESULT   4
A29671
LOCUS       A29671                    28 bp    DNA     linear   PAT 29-JUN-1995
DEFINITION  Oligonucleotide no.2.
ACCESSION   A29671
VERSION     A29671.1  GI:1248974
KEYWORDS    .
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequence.
REFERENCE   1  (bases 1 to 28)
  AUTHORS   Wallach,D. and Brakebusch,C.
  TITLE     Multimers of the soluble forms of TNF receptors, their preparation
            and pharmaceutical compositions containing them
  JOURNAL   Patent: EP 0526905-A 2 10-FEB-1993;
            YEDA RESEARCH AND DEVELOPMENT CO. LTD
FEATURES             Location/Qualifiers
     source          1. .28
                     /organism="synthetic construct"
                     /db_xref="taxon:32630"
BASE COUNT        6 a      6 c      7 g      9 t
ORIGIN


  Query Match             1.1%;  Score 24.8;  DB 6;  Length 28;
  Best Local Similarity   92.9%;  Pred. No. 8e+05;
  Matches   26;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy    974 agtccaagctctactccattgtttgtgg 1001
          |||||||||||||  |||||||||||||
Db      1 AGTCCAAGCTCTAGACCATTGTTTGTGG 28


RESULT   5
AR096333
LOCUS       AR096333                  24 bp    DNA     linear   PAT 08-SEP-2000
DEFINITION  Sequence 4 from patent US 6007995.
ACCESSION   AR096333
VERSION     AR096333.1  GI:10025051
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 24)
  AUTHORS   Baker,B.F. and Cowsert,L.M.
  TITLE     Antisense inhibition of TNFR1 expression
  JOURNAL   Patent: US 6007995-A 4 28-DEC-1999;
FEATURES             Location/Qualifiers
     source          1. .24
                     /organism="unknown"
BASE COUNT        7 a      7 c      6 g      4 t
ORIGIN


  Query Match             1.1%;  Score 24;  DB 6;  Length 24;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+06;
  Matches   24;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    554 tcagctgctccaaatgccgaaagg 577
          ||||||||||||||||||||||||
Db      1 TCAGCTGCTCCAAATGCCGAAAGG 24


RESULT   6
A63563
LOCUS       A63563                    28 bp    DNA     linear   PAT 12-MAR-1998
DEFINITION  Sequence 4 from Patent WO9720924.
ACCESSION   A63563
VERSION     A63563.1  GI:3717218
KEYWORDS    .
SOURCE      unidentified.
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 28)
  AUTHORS   Scaggiante,B. and Quadrifoglio,F.
  TITLE     A CLASS OF OLIGONUCLEOTIDES, THERAPEUTICALLY USEFUL AS ANTITUMOURAL
```

```
            AGENTS
  JOURNAL   Patent: WO 9720924-A 4 12-JUN-1997;
            SAICOM S R L (IT)
COMMENT     Other publication IT MI952539 19970604
            Other publication AU 1175497 19970627.
FEATURES             Location/Qualifiers
     source          1. .28
                     /organism="unidentified"
                     /db_xref="taxon:32644"
BASE COUNT         0 a      0 c      6 g     22 t
ORIGIN


  Query Match           1.1%;  Score 24;  DB 6;  Length 28;
  Best Local Similarity  100.0%;  Pred. No. 1.2e+06;
  Matches   24;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy   1976 ttttgttttgttttgttttgtttt 1999
           ||||||||||||||||||||||||
Db      3 TTTTGTTTTGTTTTGTTTTGTTTT 26


RESULT   7
A26411/c
LOCUS       A26411                   29 bp    DNA     linear   PAT 25-APR-1995
DEFINITION  oligonucleotide  2 from patent EP0417563.
ACCESSION   A26411
VERSION     A26411.1  GI:904967
KEYWORDS    .
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequence.
REFERENCE   1  (bases 1 to 29)
  AUTHORS   Brockhaus,M., Dembic,Z., Gentz,R., Lesslauer,W., Loetscher,H. and
            Schlaeger,E.J.
  TITLE     TNF-binding proteins
  JOURNAL   Patent: EP 0417563-A 2 20-MAR-1991;
            F. HOFFMANN-LA ROCHE AG
FEATURES             Location/Qualifiers
     source          1. .29
                     /organism="synthetic construct"
                     /db_xref="taxon:32630"
BASE COUNT         5 a      7 c      9 g      8 t
ORIGIN


  Query Match           1.1%;  Score 23.8;  DB 6;  Length 29;
  Best Local Similarity  92.6%;  Pred. No. 1.3e+06;
  Matches   25;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy    869 ctgaggactcaggcaccacagtgctgt 895
          |||||||||||||||||||| ||| |
Db     29 CTGAGGACTCAGGCACCACAGAGCTCT 3


RESULT   8
A39497/c
LOCUS       A39497                   23 bp    DNA     linear   PAT 05-MAR-1997
DEFINITION  Sequence 1 from Patent EP0606869.
ACCESSION   A39497
VERSION     A39497.1  GI:2295815
KEYWORDS    .
SOURCE      unidentified.
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 23)
  AUTHORS   Wallach,D. and Kemper,O.
  TITLE     Promotor sequence of the p55 tumor necrosis factor receptor
  JOURNAL   Patent: EP 0606869-A 1 20-JUL-1994;
            YEDA RES & DEV (IL)
COMMENT     Other publication JP 7046987 950221
            Other publication CA 2113023 940711
            Other publication AU 5307994 940714
            Other publication ZA 9400129 940819.
FEATURES             Location/Qualifiers
     source          1. .23
                     /organism="unidentified"
                     /db_xref="taxon:32644"
BASE COUNT         5 a      2 c     10 g      6 t
ORIGIN


  Query Match           1.1%;  Score 23;  DB 6;  Length 23;
  Best Local Similarity  100.0%;  Pred. No. 1.8e+06;
  Matches   23;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    122 agtctcaaccctcaactgtcacc 144
          |||||||||||||||||||||||
Db     23 AGTCTCAACCCTCAACTGTCACC 1


RESULT
AR096331
LOCUS       AR096331                 23 bp    DNA     linear   PAT 08-SEP-2000
DEFINITION  Sequence 2 from patent US 6007995.
ACCESSION   AR096331
VERSION     AR096331.1  GI:10025047
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 23)
  AUTHORS   Baker,B.F. and Cowsert,L.M.
  TITLE     Antisense inhibition of TNFR1 expression
  JOURNAL   Patent: US 6007995-A 2 28-DEC-1999;
FEATURES             Location/Qualifiers
     source          1. .23
                     /organism="unknown"
BASE COUNT         9 a      8 c      3 g      3 t
ORIGIN


  Query Match           1.1%;  Score 23;  DB 6;  Length 23;
  Best Local Similarity  100.0%;  Pred. No. 1.8e+06;
  Matches   23;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    526 gcttcagaaaaccacctcagaca 548
          |||||||||||||||||||||||
Db      1 GCTTCAGAAAACCACCTCAGACA 23


RESULT  10
AR131318
LOCUS       AR131318                 27 bp    DNA     linear   PAT 16-MAY-2001
DEFINITION  Sequence 18 from patent US 6193972.
ACCESSION   AR131318
VERSION     AR131318.1  GI:14120221
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 27)
  AUTHORS   Campbell,R.K., Jameson,B.A. and Chappel,S.C.
  TITLE     Hybrid heterodimeric protein hormone
  JOURNAL   Patent: US 6193972-A 18 27-FEB-2001;
FEATURES             Location/Qualifiers
     source          1. .27
                     /organism="unknown"
BASE COUNT         5 a      6 c      5 g     11 t
ORIGIN


  Query Match           1.1%;  Score 23;  DB 6;  Length 27;
  Best Local Similarity  100.0%;  Pred. No. 1.8e+06;
  Matches   23;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
```

```
Qy     593 agatctcttcttgcacagtggac 615
           |||||||||||||||||||||||
Db       5 AGATCTCTTCTTGCACAGTGGAC 27


RESULT  11
AR134770
LOCUS       AR134770                  27 bp    DNA     linear   PAT 16-MAY-2001
DEFINITION  Sequence 18 from patent US 6194177.
ACCESSION   AR134770
VERSION     AR134770.1  GI:14123675
KEYWORDS
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 27)
  AUTHORS   Campbell,R.K., Jameson,B.A. and Chappel,S.C.
  TITLE     DNA encoding a hybrid heterodimeric protein
  JOURNAL   Patent: US 6194177-A 18 27-FEB-2001;
FEATURES             Location/Qualifiers
     source          1. .27
                     /organism="unknown"
BASE COUNT        5 a      6 c      5 g     11 t
ORIGIN


  Query Match             1.1%;  Score 23;  DB 6;  Length 27;
  Best Local Similarity   100.0%;  Pred. No. 1.8e+06;
  Matches   23;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     593 agatctcttcttgcacagtggac 615
           |||||||||||||||||||||||
Db       5 AGATCTCTTCTTGCACAGTGGAC 27


RESULT  12
A29670
LOCUS       A29670                    26 bp    DNA     linear   PAT 29-JUN-1995
DEFINITION  Oligonucleotide no.1.
ACCESSION   A29670
VERSION     A29670.1  GI:1248973
KEYWORDS    .
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequence.
REFERENCE   1  (bases 1 to 26)
  AUTHORS   Wallach,D. and Brakebusch,C.
  TITLE     Multimers of the soluble forms of TNF receptors, their preparation
            and pharmaceutical compositions containing them
  JOURNAL   Patent: EP 0526905-A 1 10-FEB-1993;
            YEDA RESEARCH AND DEVELOPMENT CO. LTD
FEATURES             Location/Qualifiers
     source          1. .26
                     /organism="synthetic construct"
                     /db_xref="taxon:32630"
BASE COUNT        6 a      10 c      7 g      3 t
ORIGIN


  Query Match             1.1%;  Score 22.8;  DB 6;  Length 26;
  Best Local Similarity   92.3%;  Pred. No. 2e+06;
  Matches   24;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy    1257 ccccaaccccccttcagaagtgggagg 1282
           ||||||||||||  ||||||||||||
Db       1 CCCCAACCCCCTCTAGAAGTGGGAGG 26


RESULT  13
A43784/c
LOCUS       A43784                    30 bp    DNA     linear   PAT 06-MAR-1997
DEFINITION  Sequence 9 from Patent WO9508000.
ACCESSION   A43784
VERSION     A43784.1  GI:2298962
KEYWORDS    .
SOURCE      unidentified.
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 30)
  AUTHORS   Mandrand,B., Cros,P., Delair,T., Charles,M., Erout,M. and Pichot,C.
  TITLE     REAGENT AND METHOD FOR THE DETECTION OF A NUCLEOTIDE SEQUENCE WITH
            SIGNAL AMPLIFICATION
  JOURNAL   Patent: WO 9508000-A 9 23-MAR-1995;
            BIO MERIEUX (FR)
COMMENT     Other publication CA 2149315 950323
            Other publication FR 2710075 950324.
FEATURES             Location/Qualifiers
     source          1. .30
                     /organism="unidentified"
                     /db_xref="taxon:32644"
BASE COUNT       30 a      0 c      0 g      0 t
ORIGIN


  Query Match             1.0%;  Score 22.6;  DB 6;  Length 30;
  Best Local Similarity   86.2%;  Pred. No. 2.2e+06;
  Matches   25;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy    1966 ttttttttgtttttgttttgttttgtttt 1994
           ||||||||  |||||  ||||  ||||  ||||
Db      30 TTTTTTTTTTTTTTTTTTTTTTTTTTTTT 2


RESULT  14
A62991
LOCUS       A62991                    30 bp    DNA     linear   PAT 12-MAR-1998
DEFINITION  Sequence 3 from Patent WO9720068.
ACCESSION   A62991
VERSION     A62991.1  GI:3716863
KEYWORDS    .
SOURCE      unidentified.
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 30)
  AUTHORS   Oerum,H. and Seeger,C.
  TITLE     METHOD FOR GENERATING MULTIPLE DOUBLE STRANDED NUCLEIC ACIDS
  JOURNAL   Patent: WO 9720068-A 3 05-JUN-1997;
            BOEHRINGER MANNHEIM GMBH (DE)
FEATURES             Location/Qualifiers
     source          1. .30
                     /organism="unidentified"
                     /db_xref="taxon:32644"
BASE COUNT        0 a      0 c      0 g     30 t
ORIGIN


  Query Match             1.0%;  Score 22.6;  DB 6;  Length 30;
  Best Local Similarity   86.2%;  Pred. No. 2.2e+06;
  Matches   25;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy    1966 ttttttttgtttttgttttgttttgtttt 1994
           ||||||||  |||||  ||||  ||||  ||||
Db       1 TTTTTTTTTTTTTTTTTTTTTTTTTTTTT 29


RESULT  15
A62995/c
LOCUS       A62995                    30 bp    DNA     linear   PAT 12-MAR-1998
DEFINITION  Sequence 7 from Patent WO9720068.
ACCESSION   A62995
VERSION     A62995.1  GI:3716867
KEYWORDS    .
SOURCE      unidentified.
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 30)
```

AUTHORS Oerum,H. and Seeger,C.
TITLE METHOD FOR GENERATING MULTIPLE DOUBLE STRANDED NUCLEIC ACIDS
JOURNAL Patent: WO 9720068-A 7 05-JUN-1997;
BOEHRINGER MANNHEIM GMBH (DE)
FEATURES Location/Qualifiers
source 1. .30
/organism="unidentified"
/db_xref="taxon:32644"
BASE COUNT 30 a 0 c 0 g 0 t
ORIGIN

Query Match 1.0%; Score 22.6; DB 6; Length 30;
Best Local Similarity 86.2%; Pred. No. 2.2e+06;
Matches 25; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1966 ttttttttgtttttgttttgttttgtttt 1994
|||||||| ||||| |||| |||| ||||
Db 30 TTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 2

Search completed: September 19, 2002, 03:02:07
Job time: 11792 sec

GenCore version 4.5

OM nucleic - nucleic search, using sw model

Run on: September 19, 2002, 01:03:55 ; Search time 91.01 Seconds
(without alignments)
5832.480 Million cell updates/sec

Title: US-09-695-451-1
Perfect score: 2161
Sequence: 1 cggcccagtgatcttgaacc.....tacactaaaattctgaagtt 2161

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 383533 seqs, 122816752 residues

Total number of hits satisfying chosen parameters: 403436

Minimum DB seq length: 0
Maximum DB seq length: 30

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_NA:*
1: /cgn2_6/ptodata/2/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/2/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/2/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/2/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	28	1.3	28	2	US-08-859-998-261	Sequence 261, App
c	2	28	1.3	28	2	US-08-859-998-262	Sequence 262, App
	3	28	1.3	28	4	US-09-225-928-261	Sequence 261, App
c	4	28	1.3	28	4	US-09-225-928-262	Sequence 262, App
	5	25	1.2	25	4	US-09-149-922-41	Sequence 41, Appl
	6	24	1.1	24	3	US-09-106-038A-4	Sequence 4, Appli
	7	23	1.1	23	3	US-09-106-038A-2	Sequence 2, Appli
	8	23	1.1	27	4	US-08-804-166-18	Sequence 18, Appl
	9	23	1.1	27	4	US-08-910-991-18	Sequence 18, Appl
c	10	22.6	1.0	30	1	US-08-433-505-9	Sequence 9, Appli
c	11	22.6	1.0	30	3	US-08-870-730-9	Sequence 9, Appli
	12	22.6	1.0	30	4	US-09-083-123-3	Sequence 3, Appli
c	13	22.6	1.0	30	4	US-09-083-123-7	Sequence 7, Appli
c	14	22.6	1.0	30	4	US-08-882-649A-10	Sequence 10, Appl
c	15	22	1.0	30	1	US-08-068-747-6	Sequence 6, Appli
	16	22	1.0	30	1	US-08-068-747-11	Sequence 11, Appl
c	17	22	1.0	30	2	US-08-863-639A-30	Sequence 30, Appl
c	18	22	1.0	30	4	US-09-135-994-4	Sequence 4, Appli
c	19	21.8	1.0	25	1	US-08-113-646A-42	Sequence 42, Appl
c	20	21.8	1.0	25	4	US-09-149-922-42	Sequence 42, Appl
c	21	21.6	1.0	29	4	US-09-244-794A-8	Sequence 8, Appli
c	22	21.6	1.0	29	4	US-09-007-005-8	Sequence 8, Appli
c	23	21.6	1.0	29	4	US-09-247-190-8	Sequence 8, Appli
c	24	21.6	1.0	29	4	US-09-244-796-8	Sequence 8, Appli
c	25	21.6	1.0	30	1	US-08-455-627-12	Sequence 12, Appl
c	26	21.6	1.0	30	2	US-08-689-856-12	Sequence 12, Appl
c	27	21.6	1.0	30	4	US-08-787-321-12	Sequence 12, Appl
c	28	21.4	1.0	23	2	US-08-637-115-3	Sequence 3, Appli
	29	21.2	1.0	30	1	US-07-862-495-4	Sequence 4, Appli
c	30	21	1.0	21	4	US-08-804-166-19	Sequence 19, Appl
c	31	21	1.0	21	4	US-08-910-991-19	Sequence 19, Appl
	32	21	1.0	27	1	US-08-126-016-6	Sequence 6, Appli
	33	21	1.0	29	3	US-08-910-632-6	Sequence 6, Appli
	34	21	1.0	29	3	US-08-805-631A-6	Sequence 6, Appli
	35	20.8	1.0	24	2	US-08-529-190B-7	Sequence 7, Appli
c	36	20.6	1.0	27	1	US-08-208-486-79	Sequence 79, Appl
	37	20.2	0.9	26	1	US-08-621-914A-3	Sequence 3, Appli
c	38	20.2	0.9	26	3	US-08-910-632-5	Sequence 5, Appli
c	39	20.2	0.9	26	3	US-08-805-631A-5	Sequence 5, Appli
	40	20	0.9	20	1	US-08-050-319B-7	Sequence 7, Appli
	41	20	0.9	20	1	US-08-050-319B-16	Sequence 16, Appl
	42	20	0.9	20	2	US-08-465-982-7	Sequence 7, Appli
	43	20	0.9	20	2	US-08-465-982-16	Sequence 16, Appl
c	44	20	0.9	20	4	US-09-407-675-2	Sequence 2, Appli
c	45	20	0.9	30	1	US-08-050-319B-15	Sequence 15, Appl

ALIGNMENTS

```
RESULT 1
US-08-859-998-261
; Sequence 261, Application US/08859998
; Patent No. 5994076
;  GENERAL INFORMATION:
;    APPLICANT:  Chenchik, Alex
;    APPLICANT:  Jokhadze, George
;    APPLICANT:  Bibilashvilli, Robert
;    TITLE OF INVENTION:  METHOD OF ASSAYING DIFFERENTIAL
;    TITLE OF INVENTION:  EXPRESSION
;    NUMBER OF SEQUENCES:  1375
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Fish & Richardson, P.C.
;      STREET:  2200 Sand Hill Road, Suite 100
;      CITY:  Menlo Park
;      STATE:  CA
;      COUNTRY:  US
;      ZIP:  94025
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  Windows95
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/859,998
;      FILING DATE:  21-MAY-1997
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Field, Bret E.
;      REGISTRATION NUMBER:  37,620
;      REFERENCE/DOCKET NUMBER:  09096/002001
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415-322-5070
;      TELEFAX:  415-854-0875
;  INFORMATION FOR SEQ ID NO:  261:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  28 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA
;    FEATURE:
;      OTHER INFORMATION:  oligonucleotide primer
US-08-859-998-261


  Query Match                 1.3%;  Score 28;  DB 2;  Length 28;
```

```
  Best Local Similarity   100.0%;  Pred. No. 1.4e+02;
  Matches   28;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy   1645 tctaaggaccgtcctgcgagatcgcctt 1672
          ||||||||||||||||||||||||||||
Db      1 TCTAAGGACCGTCCTGCGAGATCGCCTT 28


RESULT   2
US-08-859-998-262/c
; Sequence 262, Application US/08859998
; Patent No. 5994076
;  GENERAL INFORMATION:
;    APPLICANT: Chenchik, Alex
;    APPLICANT: Jokhadze, George
;    APPLICANT: Bibilashvilli, Robert
;    TITLE OF INVENTION:  METHOD OF ASSAYING DIFFERENTIAL
;    TITLE OF INVENTION:  EXPRESSION
;    NUMBER OF SEQUENCES:  1375
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Fish & Richardson, P.C.
;      STREET:  2200 Sand Hill Road, Suite 100
;      CITY:  Menlo Park
;      STATE:  CA
;      COUNTRY:  US
;      ZIP:  94025
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  Windows95
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/859,998
;      FILING DATE:  21-MAY-1997
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Field, Bret E.
;      REGISTRATION NUMBER:  37,620
;      REFERENCE/DOCKET NUMBER:  09096/002001
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415-322-5070
;      TELEFAX:  415-854-0875
;  INFORMATION FOR SEQ ID NO:  262:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  28 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA
;    FEATURE:
;      OTHER INFORMATION:  oligonucleotide primer
US-08-859-998-262


  Query Match             1.3%;  Score 28;  DB 2;  Length 28;
  Best Local Similarity   100.0%;  Pred. No. 1.4e+02;
  Matches   28;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy   1864 tgagggacgctatgcctcatgcccgttt 1891
          ||||||||||||||||||||||||||||
Db     28 TGAGGGACGCTATGCCTCATGCCCGTTT 1


RESULT   3
US-09-225-928-261
; Sequence 261, Application US/09225928
; Patent No. 6352829
;  GENERAL INFORMATION:
;       APPLICANT: Chenchik, Alex
;                  Jokhadze, George
;                  Bibilashvilli, Robert
;       TITLE OF INVENTION: METHOD OF ASSAYING DIFFERENTIAL
;                           EXPRESSION
;       NUMBER OF SEQUENCES: 1375
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Fish & Richardson, P.C.
;            STREET: 2200 Sand Hill Road, Suite 100
;            CITY: Menlo Park
;            STATE: CA
;            COUNTRY: US
;            ZIP: 94025
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Diskette
;            COMPUTER: IBM Compatible
;            OPERATING SYSTEM: Windows95
;            SOFTWARE: FastSEQ for Windows Version 2.0
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/09/225,928
;            FILING DATE: 05-Jan-1999
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: 08/859,998
;            FILING DATE: 21-MAY-1997
;       ATTORNEY/AGENT INFORMATION:
;            NAME: Field, Bret E.
;            REGISTRATION NUMBER: 37,620
;            REFERENCE/DOCKET NUMBER: 09096/002001
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: 415-322-5070
;            TELEFAX: 415-854-0875
;  INFORMATION FOR SEQ ID NO: 261:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 28 base pairs
;            TYPE: nucleic acid
;            STRANDEDNESS: single
;            TOPOLOGY: linear
;       MOLECULE TYPE: DNA
;       FEATURE:
;            OTHER INFORMATION:  oligonucleotide primer
;       SEQUENCE DESCRIPTION: SEQ ID NO: 261:
US-09-225-928-261


  Query Match             1.3%;  Score 28;  DB 4;  Length 28;
  Best Local Similarity   100.0%;  Pred. No. 1.4e+02;
  Matches   28;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy   1645 tctaaggaccgtcctgcgagatcgcctt 1672
          ||||||||||||||||||||||||||||
Db      1 TCTAAGGACCGTCCTGCGAGATCGCCTT 28


RESULT   4
US-09-225-928-262/c
; Sequence 262, Application US/09225928
; Patent No. 6352829
;  GENERAL INFORMATION:
;       APPLICANT: Chenchik, Alex
;                  Jokhadze, George
;                  Bibilashvilli, Robert
;       TITLE OF INVENTION: METHOD OF ASSAYING DIFFERENTIAL
;                           EXPRESSION
;       NUMBER OF SEQUENCES: 1375
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Fish & Richardson, P.C.
;            STREET: 2200 Sand Hill Road, Suite 100
;            CITY: Menlo Park
;            STATE: CA
;            COUNTRY: US
;            ZIP: 94025
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Diskette
;            COMPUTER: IBM Compatible
```

```
;            OPERATING SYSTEM: Windows95
;            SOFTWARE: FastSEQ for Windows Version 2.0
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/09/225,928
;            FILING DATE: 05-Jan-1999
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: 08/859,998
;            FILING DATE: 21-MAY-1997
;       ATTORNEY/AGENT INFORMATION:
;            NAME: Field, Bret E.
;            REGISTRATION NUMBER: 37,620
;            REFERENCE/DOCKET NUMBER: 09096/002001
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: 415-322-5070
;            TELEFAX: 415-854-0875
;   INFORMATION FOR SEQ ID NO: 262:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 28 base pairs
;            TYPE: nucleic acid
;            STRANDEDNESS: single
;            TOPOLOGY: linear
;       MOLECULE TYPE: DNA
;       FEATURE:
;            OTHER INFORMATION: oligonucleotide primer
;       SEQUENCE DESCRIPTION: SEQ ID NO: 262:
US-09-225-928-262


  Query Match             1.3%;  Score 28;  DB 4;  Length 28;
  Best Local Similarity   100.0%;  Pred. No. 1.4e+02;
  Matches   28;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    1864 tgagggacgctatgcctcatgcccgttt 1891
           ||||||||||||||||||||||||||||
Db      28 TGAGGGACGCTATGCCTCATGCCCGTTT 1


RESULT   5
US-09-149-922-41
; Sequence 41, Application US/09149922A
; Patent No. 6265174
; GENERAL INFORMATION:
;  APPLICANT: Menzel, Rolf
;  APPLICANT: Hsing, Weihong
;  APPLICANT: Taggart, Pamela
;  TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR IDENTIFYING AND MODULATING
;  TITLE OF INVENTION: PROTEIN-PROTEIN INTERACTIONS
;  FILE REFERENCE: 9366-006
;  CURRENT APPLICATION NUMBER: US/09/149,922A
;  CURRENT FILING DATE: 1998-09-09
;  EARLIER APPLICATION NUMBER: 60/064,058
;  EARLIER FILING DATE: 1997-11-03
;  NUMBER OF SEQ ID NOS: 57
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 41
;   LENGTH: 25
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-149-922-41


  Query Match             1.2%;  Score 25;  DB 4;  Length 25;
  Best Local Similarity   100.0%;  Pred. No. 7.6e+02;
  Matches   25;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     248 tgtctggcatgggcctctccaccgt 272
           |||||||||||||||||||||||||
Db       1 tgtctggcatgggcctctccaccgt 25


RESULT   6
US-09-106-038A-4
; Sequence 4, Application US/09106038A
; Patent No. 6007995
;  GENERAL INFORMATION:
;    APPLICANT:  Brenda F. Baker and Lex M. Cowsert
;    TITLE OF INVENTION:  ANTISENSE MODULATION OF TNFR1
;    TITLE OF INVENTION:  EXPRESSION
;    NUMBER OF SEQUENCES:  91
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Isis Pharmaceuticals, Inc.
;      STREET:  2292 Faraday Avenue
;      CITY:  Carlsbad
;      STATE:  CA
;      COUNTRY:  U.S.A.
;      ZIP:  92008
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5 inch disk, 1.44 Mb
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  Windows NT
;      SOFTWARE:  Microsoft Word 97
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/106,038A
;      FILING DATE:  June 26, 1998
;      CLASSIFICATION:  514
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Laurel Spear Bernstein
;      REGISTRATION NUMBER:  37,280
;      REFERENCE/DOCKET NUMBER:  RTS-0004
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (760) 931-9200
;      TELEFAX:  (760) 603-3820
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  24
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-09-106-038A-4


  Query Match             1.1%;  Score 24;  DB 3;  Length 24;
  Best Local Similarity   100.0%;  Pred. No. 1.4e+03;
  Matches   24;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     554 tcagctgctccaaatgccgaaagg 577
           ||||||||||||||||||||||||
Db       1 TCAGCTGCTCCAAATGCCGAAAGG 24


RESULT   7
US-09-106-038A-2
; Sequence 2, Application US/09106038A
; Patent No. 6007995
;  GENERAL INFORMATION:
;    APPLICANT:  Brenda F. Baker and Lex M. Cowsert
;    TITLE OF INVENTION:  ANTISENSE MODULATION OF TNFR1
;    TITLE OF INVENTION:  EXPRESSION
;    NUMBER OF SEQUENCES:  91
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Isis Pharmaceuticals, Inc.
;      STREET:  2292 Faraday Avenue
;      CITY:  Carlsbad
;      STATE:  CA
;      COUNTRY:  U.S.A.
;      ZIP:  92008
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5 inch disk, 1.44 Mb
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  Windows NT
;      SOFTWARE:  Microsoft Word 97
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/106,038A
```

```
;      FILING DATE:  June 26, 1998
;      CLASSIFICATION:  514
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Laurel Spear Bernstein
;      REGISTRATION NUMBER:  37,280
;      REFERENCE/DOCKET NUMBER:  RTS-0004
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (760) 931-9200
;      TELEFAX:  (760) 603-3820
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  23
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-09-106-038A-2


  Query Match             1.1%;  Score 23;  DB 3;  Length 23;
  Best Local Similarity   100.0%;  Pred. No. 2.4e+03;
  Matches   23;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     526 gcttcagaaaaccacctcagaca 548
           |||||||||||||||||||||||
Db       1 GCTTCAGAAAACCACCTCAGACA 23


RESULT   8
US-08-804-166-18
; Sequence 18, Application US/08804166
; Patent No. 6193972
;  GENERAL INFORMATION:
;    APPLICANT:  Campbell, Robert K.
;    APPLICANT:  Jameson, Bradford A.
;    APPLICANT:  Chappel, Scott C.
;    TITLE OF INVENTION:  HYBRID PROTEINS
;    NUMBER OF SEQUENCES:  22
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  BROWDY AND NEIMARK
;      STREET:  419 Seventh Street N.W., Ste. 300
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  22207
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/804,166
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  60/011,936
;      FILING DATE:  20 February 1996
;      CLASSIFICATION:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Browdy, Roger L.
;      REGISTRATION NUMBER:  25,618
;      REFERENCE/DOCKET NUMBER:  CAMPBELL-2A
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202) 628-5197
;      TELEFAX:  (202) 737-3528
;  INFORMATION FOR SEQ ID NO:  18:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  27 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
US-08-804-166-18


  Query Match             1.1%;  Score 23;  DB 4;  Length 27;
  Best Local Similarity   100.0%;  Pred. No. 2.6e+03;
  Matches   23;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     593 agatctcttcttgcacagtggac 615
           |||||||||||||||||||||||
Db       5 AGATCTCTTCTTGCACAGTGGAC 27


RESULT   9
US-08-910-991-18
; Sequence 18, Application US/08910991
; Patent No. 6194177
;  GENERAL INFORMATION:
;    APPLICANT:  Campbell, Robert K.
;    APPLICANT:  Jameson, Bradford A.
;    APPLICANT:  Chappel, Scott C.
;    TITLE OF INVENTION:  HYBRID PROTEINS
;    NUMBER OF SEQUENCES:  22
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  BROWDY AND NEIMARK
;      STREET:  419 Seventh Street N.W., Ste. 300
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  22207
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/910,991
;      FILING DATE:
;      CLASSIFICATION:  530
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/804,166
;      FILING DATE:  20 February 1997
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  60/011,936
;      FILING DATE:  20 February 1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  YUN, Allen C.
;      REGISTRATION NUMBER:  37,971
;      REFERENCE/DOCKET NUMBER:  CAMPBELL-2B
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202) 628-5197
;      TELEFAX:  (202) 737-3528
;  INFORMATION FOR SEQ ID NO:  18:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  27 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
US-08-910-991-18


  Query Match             1.1%;  Score 23;  DB 4;  Length 27;
  Best Local Similarity   100.0%;  Pred. No. 2.6e+03;
  Matches   23;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     593 agatctcttcttgcacagtggac 615
           |||||||||||||||||||||||
Db       5 AGATCTCTTCTTGCACAGTGGAC 27


RESULT  10
US-08-433-505-9/c
; Sequence 9, Application US/08433505
; Patent No. 5695936
;  GENERAL INFORMATION:
```

```
;    APPLICANT:  MANDRAND, Bernard
;    APPLICANT:  CROS, Philippe
;    APPLICANT:  DELAIR, Thierry
;    APPLICANT:  CHARLES, Marie-Helene
;    APPLICANT:  EROUT, Marie-No. 5695936lle
;    APPLICANT:  PICHOT, Christian
;    APPLICANT:  TONNELLIER, Jean-Claude
;    TITLE OF INVENTION:  REAGENT AND METHOD FOR THE DETECTION OF
;    TITLE OF INVENTION:  A NUCLEOTIDE SEQUENCE WITH SIGNAL AMPLIFICATION
;    NUMBER OF SEQUENCES:  11
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  OLIFF & BERRIDGE
;      STREET:  P.O. Box 19928
;      CITY:  Alexandria
;      STATE:  VA
;      COUNTRY:  USA
;      ZIP:  22320
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/433,505
;      FILING DATE:  12-MAY-1995
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  BERRIDGE, WILLIAM P.
;      REGISTRATION NUMBER:  30,024
;      REFERENCE/DOCKET NUMBER:  WPB 36349
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  703-836-6400
;      TELEFAX:  703-836-2787
;  INFORMATION FOR SEQ ID NO:  9:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  30 bases
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA
US-08-433-505-9


  Query Match             1.0%;  Score 22.6;  DB 1;  Length 30;
  Best Local Similarity   86.2%;  Pred. No. 3.5e+03;
  Matches   25;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy   1966 ttttttttgtttttgttttgttttgtttt 1994
          ||||||||| ||||| |||| |||| ||||
Db     30 TTTTTTTTTTTTTTTTTTTTTTTTTTTTT 2


RESULT  11
US-08-870-730-9/c
; Sequence 9, Application US/08870730
; Patent No. 6017707
;  GENERAL INFORMATION:
;    APPLICANT:  MANDRAND, Bernard
;    APPLICANT:  CROS, Philippe
;    APPLICANT:  DELAIR, Thierry
;    APPLICANT:  CHARLES, Marie-Helene
;    APPLICANT:  EROUT, Marie-No. 601770711e
;    APPLICANT:  PICHOT, Christian
;    TITLE OF INVENTION:  REAGENT AND METHOD FOR THE DETECTION OF
;    TITLE OF INVENTION:  A NUCLEOTIDE SEQUENCE WITH SIGNAL AMPLIFICATION
;    NUMBER OF SEQUENCES:  11
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  OLIFF & BERRIDGE, PLC
;      STREET:  P.O. Box 19928
;      CITY:  Alexandria
;      STATE:  VA
;      COUNTRY:  USA
;      ZIP:  22320
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/870,730
;      FILING DATE:  06-JUN-1997
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  BERRIDGE, WILLIAM P.
;      REGISTRATION NUMBER:  30,024
;      REFERENCE/DOCKET NUMBER:  WPB 36349A
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  703-836-6400
;      TELEFAX:  703-836-2787
;  INFORMATION FOR SEQ ID NO:  9:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  30 bases
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA
US-08-870-730-9


  Query Match             1.0%;  Score 22.6;  DB 3;  Length 30;
  Best Local Similarity   86.2%;  Pred. No. 3.5e+03;
  Matches   25;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy   1966 ttttttttgtttttgttttgttttgtttt 1994
          ||||||||| ||||| |||| |||| ||||
Db     30 TTTTTTTTTTTTTTTTTTTTTTTTTTTTT 2


RESULT  12
US-09-083-123-3
; Sequence 3, Application US/09083123
; Patent No. 6326143
; GENERAL INFORMATION:
;  APPLICANT: Orum, Hendrik
;  APPLICANT: Seeger, Corina
;  TITLE OF INVENTION: Method for Generating Multiple Double Stranded Nucleic
;  TITLE OF INVENTION: Acids
;  FILE REFERENCE: sequence listing
;  CURRENT APPLICATION NUMBER: US/09/083,123
;  CURRENT FILING DATE: 1998-05-22
;  EARLIER APPLICATION NUMBER: EP 95118600.6
;  EARLIER FILING DATE: 1995-11-25
;  EARLIER APPLICATION NUMBER: PCT/EP96/05149
;  EARLIER FILING DATE: 1996-11-22
;  NUMBER OF SEQ ID NOS: 8
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
;   LENGTH: 30
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: made by humans
US-09-083-123-3


  Query Match             1.0%;  Score 22.6;  DB 4;  Length 30;
  Best Local Similarity   86.2%;  Pred. No. 3.5e+03;
  Matches   25;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy   1966 ttttttttgtttttgttttgttttgtttt 1994
          ||||||||| ||||| |||| |||| ||||
Db      1 ttttttttttttttttttttttttttttt 29


RESULT  13
US-09-083-123-7/c
```

; Sequence 7, Application US/09083123
; Patent No. 6326143
; GENERAL INFORMATION:
; APPLICANT: Orum, Hendrik
; APPLICANT: Seeger, Corina
; TITLE OF INVENTION: Method for Generating Multiple Double Stranded Nucleic
; TITLE OF INVENTION: Acids
; FILE REFERENCE: sequence listing
; CURRENT APPLICATION NUMBER: US/09/083,123
; CURRENT FILING DATE: 1998-05-22
; EARLIER APPLICATION NUMBER: EP 95118600.6
; EARLIER FILING DATE: 1995-11-25
; EARLIER APPLICATION NUMBER: PCT/EP96/05149
; EARLIER FILING DATE: 1996-11-22
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
; LENGTH: 30
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: made by humans
US-09-083-123-7

Query Match 1.0%; Score 22.6; DB 4; Length 30;
Best Local Similarity 86.2%; Pred. No. 3.5e+03;
Matches 25; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1966 ttttttttgtttttgttttgttttgtttt 1994
||||||||| ||||| |||| |||| ||||
Db 30 TTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 2

RESULT 14
US-08-882-649A-10/c
; Sequence 10, Application US/08882649A
; Patent No. 6344316
; GENERAL INFORMATION:
; APPLICANT: Lockhart, David J.
; Chee, Mark
; Gunderson, Kevin
; Chaoqiang, Lai
; Wodicka, Lisa
; Cronin, Maureen T.
; Lee, Danny
; Tran, Huu M.
; Matsuzaki, Hajime
; McGall, Glenn H.
; TITLE OF INVENTION: NUCLEIC ACID ANALYSIS TECHNIQUES
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Joe Liebeschuetz
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/882,649A
; FILING DATE: 25-Jun-1997
; CLASSIFICATION: 435-006.000
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/010,471
; FILING DATE: 23-JAN-1996
; APPLICATION NUMBER: US 60/035,170
; FILING DATE: 09-JAN-1997
; APPLICATION NUMBER: PCT/US97/01603
; FILING DATE: 22-JAN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Liebeschuetz, Joe
; REGISTRATION NUMBER: 37,505
; REFERENCE/DOCKET NUMBER: 018547-019410US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 30 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: YES
; (ix) Features:
; SEQUENCE DESCRIPTION: SEQ ID NO: 10:
US-08-882-649A-10

Query Match 1.0%; Score 22.6; DB 4; Length 30;
Best Local Similarity 86.2%; Pred. No. 3.5e+03;
Matches 25; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1966 ttttttttgtttttgttttgttttgtttt 1994
||||||||| ||||| |||| |||| ||||
Db 30 TTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 2

RESULT 15
US-08-068-747-6/c
; Sequence 6, Application US/08068747
; Patent No. 5695933
; GENERAL INFORMATION:
; APPLICANT: Schalling, Martin
; APPLICANT: Hudson, Thomas J.
; APPLICANT: Housman, David E.
; TITLE OF INVENTION: Direct Determination of Expanded
; TITLE OF INVENTION: Nucleotide Repeats in the Human Genome
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: Massachusett
; COUNTRY: USA
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/068,747
; FILING DATE: 28-MAY-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Granahan, Patricia
; REGISTRATION NUMBER: 32,227
; REFERENCE/DOCKET NUMBER: MIT-6141
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-861-6240
; TELEFAX: 617-861-9540
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 30 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "Synthetic"
US-08-068-747-6

Query Match 1.0%; Score 22; DB 1; Length 30;
Best Local Similarity 83.3%; Pred. No. 5e+03;
Matches 25; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

```
Qy    280 ctgctgctgccgctggtgctcctggagctg 309
          ||||| |||| |||| |||  ||||
Db     30 CTGCTGCTGCTGCTGCTGCTGCTGCTG 1
```

Search completed: September 19, 2002, 03:03:50
Job time: 7195 sec

GenCore version 4.5

OM nucleic - nucleic search, using sw model

Run on: September 18, 2002, 23:38:00 ; Search time 2281.52 Seconds
(without alignments)
12783.986 Million cell updates/sec

Title: US-09-695-451-1
Perfect score: 2161
Sequence: 1 cggcccagtgatcttgaacc.....tacactaaaattctgaagtt 2161

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 13736207 seqs, 6748477542 residues

Total number of hits satisfying chosen parameters: 28088

Minimum DB seq length: 0
Maximum DB seq length: 30

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_htc:*
9: gb_est1:*
10: gb_est2:*
11: gb_htc:*
12: gb_gss:*
13: em_gss_hum:*
14: em_gss_inv:*
15: em_gss_pln:*
16: em_gss_vrt:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	24	1.1	26	12	AZ771474	AZ771474 1M0573I08
	2	23.6	1.1	30	12	AZ458127	AZ458127 1M0261I24
	3	22.8	1.1	28	12	AZ419708	AZ419708 1M0196A04
c	4	22.6	1.0	29	12	AZ389566	AZ389566 1M0150D21
	5	22.6	1.0	29	12	AZ414283	AZ414283 1M0188G12
	6	22.6	1.0	29	12	AZ451930	AZ451930 1M0251E05
	7	22.6	1.0	29	12	AZ468402	AZ468402 1M0281G24
	8	22.6	1.0	29	12	AZ486793	AZ486793 1M0315N21
	9	22.6	1.0	29	12	AZ661709	AZ661709 1M0540K20
c	10	22.6	1.0	29	12	AZ784208	AZ784208 2M0026I13
c	11	22.6	1.0	29	12	AZ806470	AZ806470 2M0068I02
c	12	22.6	1.0	29	12	AZ812242	AZ812242 2M0078J15
c	13	22.6	1.0	29	12	AZ868731	AZ868731 2M0180L02
	14	22.6	1.0	29	12	TA334G09Q	AL491938 T. brucei
c	15	22.6	1.0	30	2	HSM003126	A1038650 Homo sapi
c	16	22.6	1.0	30	10	BG666435	BG666435 DRACRC02
c	17	22.6	1.0	30	10	BG865511	BG865511 602783643
	18	22.6	1.0	30	12	AZ357603	AZ357603 1M0099H17
c	19	22.6	1.0	30	12	AZ455741	AZ455741 1M0258D16
	20	22.6	1.0	30	12	AZ481739	AZ481739 1M0306N12
	21	22.6	1.0	30	12	AZ582114	AZ582114 1M0374J17
c	22	22	1.0	30	12	AZ443322	AZ443322 1M0237L20
	23	21.6	1.0	28	9	AW332443	AW332443 S8E7 AGS-
	24	21.6	1.0	28	12	AZ399637	AZ399637 1M0165N04
c	25	21.6	1.0	28	12	AZ401766	AZ401766 1M0168O08
	26	21.6	1.0	28	12	AZ471744	AZ471744 1M0286K08
	27	21.6	1.0	28	12	AZ481286	AZ481286 1M0303L24
c	28	21.6	1.0	28	12	AZ493138	AZ493138 1M0327F02
	29	21.6	1.0	28	12	AZ653365	AZ653365 1M0527E02
	30	21.6	1.0	28	12	AZ785035	AZ785035 2M0028J01
	31	21.6	1.0	28	12	AZ824519	AZ824519 2M0099I09
c	32	21.6	1.0	28	12	AZ833425	AZ833425 2M0115D04
	33	21.6	1.0	28	12	AZ866569	AZ866569 2M0177B08
c	34	21.6	1.0	28	12	TA291A01Q	AL486613 T. brucei
	35	21.6	1.0	28	12	TA379D11P	AL497637 T. brucei
c	36	21.6	1.0	30	2	HSM003148	A1038672 Homo sapi
	37	21.4	1.0	29	12	AZ492630	AZ492630 1M0326B22
c	38	21.2	1.0	27	12	TA257B07P	AL483278 T. brucei
	39	21.2	1.0	28	10	T52836	T52836 ya81b09.s1
c	40	21	1.0	29	12	AZ825156	AZ825156 2M0100N08
c	41	20.6	1.0	27	9	AW327923	AW327923 dr02g08.x
	42	20.6	1.0	27	12	AZ344642	AZ344642 1M0078H15
	43	20.6	1.0	27	12	AZ401672	AZ401672 1M0168K04
c	44	20.6	1.0	27	12	AZ434285	AZ434285 1M0220B08
c	45	20.6	1.0	27	12	AZ458228	AZ458228 1M0262C12

ALIGNMENTS

RESULT 1
AZ771474
LOCUS AZ771474 26 bp DNA linear GSS 16-FEB-2001
DEFINITION 1M0573I08R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0573I08 R, DNA sequence.
ACCESSION AZ771474
VERSION AZ771474.1 GI:12893772
KEYWORDS GSS.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 26)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0573 row: I column: 08
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 26.
FEATURES Location/Qualifiers
source 1. .26
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0573I08"
/clone_lib="Mouse 10kb plasmid UUGC1M library"

/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
BASE COUNT 0 a 0 c 6 g 20 t
ORIGIN

Query Match 1.1%; Score 24; DB 12; Length 26;
Best Local Similarity 100.0%; Pred. No. 3.6e+06;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1976 ttttgttttgttttgttttgtttt 1999
||||||||||||||||||||||||
Db 2 TTTTGTTTTGTTTTGTTTTGTTTT 25

RESULT 2
AZ458127
LOCUS AZ458127 30 bp DNA linear GSS 04-OCT-2000
DEFINITION 1M0261I24R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0261I24 R, DNA sequence.
ACCESSION AZ458127
VERSION AZ458127.1 GI:10616252
KEYWORDS GSS.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 30)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0261 row: I column: 24
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 30.
FEATURES Location/Qualifiers
source 1. .30
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0261I24"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
BASE COUNT 0 a 0 c 1 g 29 t
ORIGIN

Query Match 1.1%; Score 23.6; DB 12; Length 30;
Best Local Similarity 86.7%; Pred. No. 4.1e+06;
Matches 26; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1968 ttttttgttttttgttttgttttgttttgtt 1997
|||||| ||||| |||| ||||||||| ||
Db 1 TTTTTTTTTTTTTTTTTTTTTGTTTTTTT 30

RESULT 3
AZ419708
LOCUS AZ419708 28 bp DNA linear GSS 03-OCT-2000
DEFINITION 1M0196A04R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0196A04 R, DNA sequence.
ACCESSION AZ419708
VERSION AZ419708.1 GI:10543817
KEYWORDS GSS.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 28)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0196 row: A column: 04
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 28.
FEATURES Location/Qualifiers
source 1. .28
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"

/clone="UUGC1M0196A04"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
BASE COUNT 0 a 0 c 6 g 22 t
ORIGIN

Query Match 1.1%; Score 22.8; DB 12; Length 28;
Best Local Similarity 92.3%; Pred. No. 5.5e+06;
Matches 24; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1966 ttttttttgtttttgttttgttttgt 1991
|| ||||||||||||||| ||||||||
Db 3 TTGTTTTTGTTTTTGTTGTGTTTTGT 28

RESULT 4
AZ389566/c
LOCUS AZ389566 29 bp DNA linear GSS 02-OCT-2000
DEFINITION 1M0150D21F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0150D21 F, DNA sequence.
ACCESSION AZ389566
VERSION AZ389566.1 GI:10503274
KEYWORDS GSS.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 29)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0150 row: D column: 21
Seq primer: CGTTGTAAAACGACGGCCAGT
Class: plasmid ends
High quality sequence stop: 29.
FEATURES Location/Qualifiers
source 1. .29
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0150D21"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
BASE COUNT 29 a 0 c 0 g 0 t
ORIGIN

Query Match 1.0%; Score 22.6; DB 12; Length 29;
Best Local Similarity 86.2%; Pred. No. 5.9e+06;
Matches 25; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1966 tttttttgtttttgttttgttttgtttt 1994
|||||||| ||||| |||| |||| ||||
Db 29 TTTTTTTTTTTTTTTTTTTTTTTTTTTT 1

RESULT 5
AZ414283
LOCUS AZ414283 29 bp DNA linear GSS 03-OCT-2000
DEFINITION 1M0188G12R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0188G12 R, DNA sequence.
ACCESSION AZ414283
VERSION AZ414283.1 GI:10538296
KEYWORDS GSS.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 29)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0188 row: G column: 12
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 29.
FEATURES Location/Qualifiers
source 1. .29
/organism="Mus musculus"

/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0188G12"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
BASE COUNT 0 a 0 c 0 g 29 t
ORIGIN

Query Match 1.0%; Score 22.6; DB 12; Length 29;
Best Local Similarity 86.2%; Pred. No. 5.9e+06;
Matches 25; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1966 ttttttttgtttttgttttgttttgtttt 1994
||||||||.|||||.||||.||||.||||
Db 1 TTTTTTTTTTTTTTTTTTTTTTTTTTTTT 29

RESULT 6
AZ451930
LOCUS AZ451930 29 bp DNA linear GSS 04-OCT-2000
DEFINITION 1M0251E05R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0251E05 R, DNA sequence.
ACCESSION AZ451930
VERSION AZ451930.1 GI:10608203
KEYWORDS GSS.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 29)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0251 row: E column: 05
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 29.
FEATURES Location/Qualifiers
source 1. .29

/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0251E05"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
BASE COUNT 0 a 0 c 0 g 29 t
ORIGIN

Query Match 1.0%; Score 22.6; DB 12; Length 29;
Best Local Similarity 86.2%; Pred. No. 5.9e+06;
Matches 25; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1966 ttttttttgtttttgttttgttttgtttt 1994
||||||||.|||||.||||.||||.||||
Db 1 TTTTTTTTTTTTTTTTTTTTTTTTTTTTT 29

RESULT 7
AZ468402
LOCUS AZ468402 29 bp DNA linear GSS 04-OCT-2000
DEFINITION 1M0281G24F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0281G24 F, DNA sequence.
ACCESSION AZ468402
VERSION AZ468402.1 GI:10626527
KEYWORDS GSS.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 29)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0281 row: G column: 24
Seq primer: CGTTGTAAAACGACGGCCAGT
Class: plasmid ends
High quality sequence stop: 29.
FEATURES Location/Qualifiers

source 1. .29
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0281G24"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
BASE COUNT 0 a 0 c 0 g 29 t
ORIGIN

Query Match 1.0%; Score 22.6; DB 12; Length 29;
Best Local Similarity 86.2%; Pred. No. 5.9e+06;
Matches 25; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1966 ttttttttgtttttgttttgttttgtttt 1994
||||||||| ||||| |||| |||| ||||
Db 1 TTTTTTTTTTTTTTTTTTTTTTTTTTTTT 29

RESULT 8
AZ486793
LOCUS AZ486793 29 bp DNA linear GSS 05-OCT-2000
DEFINITION 1M0315N21F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0315N21 F, DNA sequence.
ACCESSION AZ486793
VERSION AZ486793.1 GI:10653915
KEYWORDS GSS.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 29)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0315 row: N column: 21
Seq primer: CGTTGTAAAACGACGGCCAGT
Class: plasmid ends
High quality sequence stop: 29.

FEATURES Location/Qualifiers
source 1. .29
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0315N21"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
BASE COUNT 0 a 0 c 0 g 29 t
ORIGIN

Query Match 1.0%; Score 22.6; DB 12; Length 29;
Best Local Similarity 86.2%; Pred. No. 5.9e+06;
Matches 25; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1966 ttttttttgtttttgttttgttttgtttt 1994
||||||||| ||||| |||| |||| ||||
Db 1 TTTTTTTTTTTTTTTTTTTTTTTTTTTTT 29

RESULT 9
AZ661709
LOCUS AZ661709 29 bp DNA linear GSS 14-DEC-2000
DEFINITION 1M0540K20F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0540K20 F, DNA sequence.
ACCESSION AZ661709
VERSION AZ661709.1 GI:11798855
KEYWORDS GSS.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 29)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0540 row: K column: 20
Seq primer: CGTTGTAAAACGACGGCCAGT
Class: plasmid ends

High quality sequence stop: 29.
FEATURES Location/Qualifiers
source 1. .29
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0540K20"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
BASE COUNT 0 a 0 c 0 g 29 t
ORIGIN

Query Match 1.0%; Score 22.6; DB 12; Length 29;
Best Local Similarity 86.2%; Pred. No. 5.9e+06;
Matches 25; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1966 ttttttttgtttttgttttgttttgtttt 1994
||||||||| ||||| |||| |||| ||||
Db 1 TTTTTTTTTTTTTTTTTTTTTTTTTTTTT 29

RESULT 10
AZ784208/c
LOCUS AZ784208 29 bp DNA linear GSS 16-FEB-2001
DEFINITION 2M0026I13R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC2M0026I13 R, DNA sequence.
ACCESSION AZ784208
VERSION AZ784208.1 GI:12919703
KEYWORDS GSS.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 29)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0026 row: I column: 13
Seq primer: CACACAGGAAACAGCTATGACC

Class: plasmid ends
High quality sequence stop: 29.
FEATURES Location/Qualifiers
source 1. .29
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0026I13"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
BASE COUNT 29 a 0 c 0 g 0 t
ORIGIN

Query Match 1.0%; Score 22.6; DB 12; Length 29;
Best Local Similarity 86.2%; Pred. No. 5.9e+06;
Matches 25; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1966 ttttttttgtttttgttttgttttgtttt 1994
||||||||| ||||| |||| |||| ||||
Db 29 TTTTTTTTTTTTTTTTTTTTTTTTTTTTT 1

RESULT 11
AZ806470/c
LOCUS AZ806470 29 bp DNA linear GSS 20-FEB-2001
DEFINITION 2M0068I02R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC2M0068I02 R, DNA sequence.
ACCESSION AZ806470
VERSION AZ806470.1 GI:12969849
KEYWORDS GSS.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 29)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0068 row: I column: 02

```
            Seq primer: CACACAGGAAACAGCTATGACC
            Class: plasmid ends
            High quality sequence stop: 29.
FEATURES              Location/Qualifiers
     source           1. .29
                      /organism="Mus musculus"
                      /strain="C57BL/6J"
                      /db_xref="taxon:10090"
                      /clone="UUGC2M0068I02"
                      /clone_lib="Mouse 10kb plasmid UUGC1M library"
                      /sex="Male"
                      /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                      /note="Vector: PWD42nv; Purified genomic DNA from M.
                      musculus C57BL/6J (male) was obtained  from the Jackson
                      Laboratory Mouse DNA Resource
                      (http://www.jax.org/resources/documents/dnares/). The DNA
                      was hydrodynamically sheared by repeated passage through a
                      0.005 inch orifice at constant velocity. The sheared DNA
                      was blunt end-repaired with T4 DNA polymerase and T4
                      polynucleotide kinase. Adaptor oligonucleotides were
                      ligated to the blunt ends in high  molar excess. The
                      adaptored DNA was purified and size-selected for a 9.5 to
                      10.5 kb range using preparative agarose gel
                      electrophoresis. Vector DNA was prepared from a derivative
                      of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                      inducible derivative of plasmid R1. The vector was ligated
                      with adaptors complementary to the insert adaptors and
                      purified. The sheared, adaptored mouse DNA was annealed to
                      adaptored vector DNA, and transformed into
                      chemically-competent E. coli XL10-Gold (Stratagene) cells
                      and selected for ampicillin resistance."
BASE COUNT       29 a      0 c      0 g      0 t
ORIGIN


  Query Match             1.0%;  Score 22.6;  DB 12;  Length 29;
  Best Local Similarity   86.2%;  Pred. No. 5.9e+06;
  Matches   25;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy   1966 ttttttttgtttttgttttgttttgtttt 1994
           |||||||| ||||| |||| |||| ||||
Db     29 TTTTTTTTTTTTTTTTTTTTTTTTTTTTT 1


RESULT  12
AZ812242/c
LOCUS       AZ812242                29 bp    DNA     linear   GSS 20-FEB-2001
DEFINITION  2M0078J15R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC2M0078J15 R, DNA sequence.
ACCESSION   AZ812242
VERSION     AZ812242.1  GI:12981296
KEYWORDS    GSS.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 29)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
            ,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
            and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0078  row: J  column: 15
            Seq primer: CACACAGGAAACAGCTATGACC
            Class: plasmid ends
            High quality sequence stop: 29.
FEATURES              Location/Qualifiers
     source           1. .29
                      /organism="Mus musculus"
                      /strain="C57BL/6J"
                      /db_xref="taxon:10090"
                      /clone="UUGC2M0078J15"
                      /clone_lib="Mouse 10kb plasmid UUGC1M library"
                      /sex="Male"
                      /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                      /note="Vector: PWD42nv; Purified genomic DNA from M.
                      musculus C57BL/6J (male) was obtained  from the Jackson
                      Laboratory Mouse DNA Resource
                      (http://www.jax.org/resources/documents/dnares/). The DNA
                      was hydrodynamically sheared by repeated passage through a
                      0.005 inch orifice at constant velocity. The sheared DNA
                      was blunt end-repaired with T4 DNA polymerase and T4
                      polynucleotide kinase. Adaptor oligonucleotides were
                      ligated to the blunt ends in high  molar excess. The
                      adaptored DNA was purified and size-selected for a 9.5 to
                      10.5 kb range using preparative agarose gel
                      electrophoresis. Vector DNA was prepared from a derivative
                      of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                      inducible derivative of plasmid R1. The vector was ligated
                      with adaptors complementary to the insert adaptors and
                      purified. The sheared, adaptored mouse DNA was annealed to
                      adaptored vector DNA, and transformed into
                      chemically-competent E. coli XL10-Gold (Stratagene) cells
                      and selected for ampicillin resistance."
BASE COUNT       29 a      0 c      0 g      0 t
ORIGIN


  Query Match             1.0%;  Score 22.6;  DB 12;  Length 29;
  Best Local Similarity   86.2%;  Pred. No. 5.9e+06;
  Matches   25;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy   1966 ttttttttgtttttgttttgttttgtttt 1994
           |||||||| ||||| |||| |||| ||||
Db     29 TTTTTTTTTTTTTTTTTTTTTTTTTTTTT 1


RESULT  13
AZ868731/c
LOCUS       AZ868731                29 bp    DNA     linear   GSS 21-FEB-2001
DEFINITION  2M0180L02R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC2M0180L02 R, DNA sequence.
ACCESSION   AZ868731
VERSION     AZ868731.1  GI:13072338
KEYWORDS    GSS.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 29)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
            ,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
            and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
```

```
            Insert Length: 10000   Std Error: 0.00
            Plate: 0180  row: L  column: 02
            Seq primer: CACACAGGAAACAGCTATGACC
            Class: plasmid ends
            High quality sequence stop: 29.
FEATURES              Location/Qualifiers
     source           1. .29
                      /organism="Mus musculus"
                      /strain="C57BL/6J"
                      /db_xref="taxon:10090"
                      /clone="UUGC2M0180L02"
                      /clone_lib="Mouse 10kb plasmid UUGC1M library"
                      /sex="Male"
                      /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                      /note="Vector: PWD42nv; Purified genomic DNA from M.
                      musculus C57BL/6J (male) was obtained  from the Jackson
                      Laboratory Mouse DNA Resource
                      (http://www.jax.org/resources/documents/dnares/). The DNA
                      was hydrodynamically sheared by repeated passage through a
                      0.005 inch orifice at constant velocity. The sheared DNA
                      was blunt end-repaired with T4 DNA polymerase and T4
                      polynucleotide kinase. Adaptor oligonucleotides were
                      ligated to the blunt ends in high  molar excess. The
                      adaptored DNA was purified and size-selected for a 9.5 to
                      10.5 kb range using preparative agarose gel
                      electrophoresis. Vector DNA was prepared from a derivative
                      of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                      inducible derivative of plasmid R1. The vector was ligated
                      with adaptors complementary to the insert adaptors and
                      purified. The sheared, adaptored mouse DNA was annealed to
                      adaptored vector DNA, and transformed into
                      chemically-competent E. coli XL10-Gold (Stratagene) cells
                      and selected for ampicillin resistance."
BASE COUNT       29 a      0 c      0 g      0 t
ORIGIN


  Query Match             1.0%;  Score 22.6;  DB 12;  Length 29;
  Best Local Similarity   86.2%;  Pred. No. 5.9e+06;
  Matches   25;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy   1966 ttttttttgtttttgttttgttttgtttt 1994
           |||||||| ||||| |||| |||| ||||
Db     29 TTTTTTTTTTTTTTTTTTTTTTTTTTTTT 1


RESULT  14
TA334G09Q
LOCUS       TA334G09Q                29 bp    DNA     linear   GSS 13-DEC-2000
DEFINITION  T. brucei sheared genomic DNA clone 334g09, reverse sequence,
            genomic survey sequence.
ACCESSION   AL491938
VERSION     AL491938.1  GI:11868238
KEYWORDS    GSS.
SOURCE      Trypanosoma brucei.
  ORGANISM  Trypanosoma brucei
            Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
            Trypanosoma.
REFERENCE   1  (bases 1 to 29)
  AUTHORS   Hall,N., Bowman,S., Lennard,N.J., Doggett,J., Atkin,R.,
            Chillingworth,C., Ormond,D., Harris,B., El-Sayed,N., Hou,L.,
            Melville,S.E., Rajandream,M.A. and Barrell,B.G.
  TITLE     Direct Submission
  JOURNAL   Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing
            project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,
            Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and
            nh1@sanger.ac.uk
COMMENT     Constructed at the Institute for Genomic Research (TIGR),
            Rockville, MD. Genomic DNA isolated from a cloned population of
            Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared
            to give a tight size distribution (
            4 kb).  The v + i method used for the library construction is
            described in detail in Smith, H. and Venter, J.C. (Making small
            insert libraries for whole genome shotgun sequencing projects.  In
            Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.
            Barrell, Oxford University Press, 1999).
            Email: nelsayed@tigr.org
            Details of T. brucei sequencing at the Sanger Centre are available
            at http://www.sanger.ac.uk/Projects/T_brucei/.
FEATURES              Location/Qualifiers
     source           1. .29
                      /organism="Trypanosoma brucei"
                      /strain="TREU927"
                      /db_xref="taxon:5691"
                      /clone="334g09"
BASE COUNT       0 a      0 c      0 g     29 t
ORIGIN


  Query Match             1.0%;  Score 22.6;  DB 12;  Length 29;
  Best Local Similarity   86.2%;  Pred. No. 5.9e+06;
  Matches   25;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy   1966 ttttttttgtttttgttttgttttgtttt 1994
           |||||||| ||||| |||| |||| ||||
Db      1 TTTTTTTTTTTTTTTTTTTTTTTTTTTTT 29


RESULT  15
HSM003126/c
ID   HSM003126  standard; RNA; EST; 30 BP.
XX
AC   AL038650;
XX
SV   AL038650.1
XX
DT   12-MAR-1999 (Rel. 59, Created)
DT   12-MAR-1999 (Rel. 59, Last updated, Version 1)
XX
DE   Homo sapiens mRNA; EST DKFZp566I1846_r1  (from clone DKFZp566I1846)
XX
KW   EST; expressed sequence tag.
XX
OS   Homo sapiens (human)
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
OC   Eutheria; Primates; Catarrhini; Hominidae; Homo.
XX
RN   [1]
RP   1-30
RA   Ottenwaelder B., Obermaier B., Mewes W., Gassenhuber J., Wiemann S.;
RT   ;
RL   Submitted (12-MAR-1999) to the EMBL/GenBank/DDBJ databases.
RL   MIPS, Am Klopferspitz 18a D-82152 Martinsried, GERMANY
XX
CC   Clone from S. Wiemann, sequenced by MediGenomix within the cDNA
CC   sequencing consortium of the German Genome Project
CC   s1 sequence also available
CC   This clone is available at the RZPD in Berlin
CC   Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
CC   Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de
XX
FH   Key             Location/Qualifiers
FH
FT   source          1. .30
FT                   /db_xref="taxon:9606"
FT                   /organism="Homo sapiens"
FT                   /clone="DKFZp566I1846"
FT                   /clone_lib="566 (synonym: hfkd2). Vector pAMP1; host
FT                   Xl-2blue; sites NotI + SalI"
FT                   /dev_stage="fetal"
FT                   /tissue_type="kidney"
XX
SQ   Sequence 30 BP; 30 A; 0 C; 0 G; 0 T; 0 other;


  Query Match             1.0%;  Score 22.6;  DB 2;  Length 30;
```

Best Local Similarity 86.2%; Pred. No. 5.8e+06;
Matches 25; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

```
Qy   1966 ttttttttgtttttgttttgttttgtttt 1994
          ||||||||| ||||| |||| |||| |||| .
Db     30 TTTTTTTTTTTTTTTTTTTTTTTTTTTTT 2
```

Search completed: September 19, 2002, 01:56:34
Job time: 8314 sec

GenCore version 4.5

OM nucleic - nucleic search, using sw model

Run on: September 19, 2002, 01:18:25 ; Search time 358.05 Seconds
(without alignments)
10362.385 Million cell updates/sec

Title: US-09-695-451-1
Perfect score: 2161
Sequence: 1 cggcccagtgatcttgaacc.....tacactaaaattctgaagtt 2161

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1736436 seqs, 858457221 residues

Total number of hits satisfying chosen parameters: 1662488

Minimum DB seq length: 0
Maximum DB seq length: 30

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_032802:*
1: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1980.DAT:*
2: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1981.DAT:*
3: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1982.DAT:*
4: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1983.DAT:*
5: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1984.DAT:*
6: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1985.DAT:*
7: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1986.DAT:*
8: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1987.DAT:*
9: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1988.DAT:*
10: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1989.DAT:*
11: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1990.DAT:*
12: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1991.DAT:*
13: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1992.DAT:*
14: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1993.DAT:*
15: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1994.DAT:*
16: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1995.DAT:*
17: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1996.DAT:*
18: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1997.DAT:*
19: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1998.DAT:*
20: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1999.DAT:*
21: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA2000.DAT:*
22: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA2001A.DAT:*
23: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA2001B.DAT:*
24: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	27	1.2	27	20	AAZ09162	Human tumour necro
	2	27	1.2	27	22	AAH48867	Human 55 kD TNFBP
	3	25	1.2	25	20	AAX58185	Primer for CadC-fu
c	4	25	1.2	25	21	AAA95191	Reverse primer use
	5	25	1.2	30	21	AAZ50185	XbaI primer for D1
c	6	24	1.1	24	12	AAQ11261	Probe for clone en
	7	24	1.1	24	21	AAZ48478	Human TNFR1 DNA hy
c	8	24	1.1	24	22	AAC83958	Human 30 kDa TNF i
	9	24	1.1	28	18	AAT93813	Antitumoural phosp
c	10	23.8	1.1	29	20	AAZ09169	Human 55kDa tumour
c	11	23.8	1.1	29	22	AAH48858	Human 55 kD TNFBP
c	12	23	1.1	23	12	AAQ11256	Probe for clone en
c	13	23	1.1	23	15	AAQ69116	p55 TNF-R gene 5'
c	14	23	1.1	23	15	AAQ69119	p55 TNF-R gene 5'
	15	23	1.1	23	21	AAZ48476	Human TNFR1 DNA am
c	16	23	1.1	23	22	AAC83953	Human 30 kDa TNF i
	17	23	1.1	27	18	AAT94016	Primer for TPO/hCG
	18	22.6	1.0	29	11	AAQ05003	Sequence binding t
	19	22.6	1.0	30	8	AAN70277	Sequence of scissi
	20	22.6	1.0	30	10	AAN92243	SS probe MRCO64.
	21	22.6	1.0	30	14	AAQ36301	GST3par, for GSTpi
	22	22.6	1.0	30	14	AAQ36302	GST3anti, for GSTp
	23	22.6	1.0	30	20	AAX57020	WO9923258 oligonuc
	24	22.6	1.0	30	22	AAF99888	Immunostimulatory
c	25	22.6	1.0	30	22	AAF99889	Immunostimulatory
c	26	22	1.0	22	22	AAD16934	Human TNF-R1 (p55)
c	27	22	1.0	30	21	AAZ44310	Human SCA7 primer
c	28	21.8	1.0	25	20	AAX58186	Primer for CadC-fu
c	29	21.6	1.0	29	21	AAA94315	RNA-protein fusion
c	30	21.6	1.0	29	22	AAH20990	C-myc epitope puro
c	31	21.6	1.0	29	22	AAS00066	Synthetic branched
c	32	21.6	1.0	30	16	AAQ83940	Oligonucleotide cl
c	33	21.6	1.0	30	19	AAV48087	Oligonucleotide 30
c	34	21.6	1.0	30	22	AAF60462	Oligonucleotide cl
c	35	21.4	1.0	23	21	AAZ39413	Forward primer amp
	36	21.2	1.0	28	21	AAA40358	pBluescriptSK+ pha
	37	21.2	1.0	30	16	AAT03314	Human TNF receptor
	38	21.2	1.0	30	16	AAQ84732	Primer to clone th
c	39	21	1.0	21	18	AAT94017	Primer for TPO/hCG
	40	21	1.0	21	22	AAF96710	Human gene single
	41	21	1.0	21	22	AAF96711	Human gene single
	42	21	1.0	29	19	AAV59216	Linear multimer pr
	43	21	1.0	30	19	AAV19815	PCR primer for tru
	44	21	1.0	30	19	AAV19819	PCR primer for tru
	45	20.8	1.0	24	19	AAV55815	Multimerisation of

ALIGNMENTS

RESULT 1
AAZ09162
ID AAZ09162 standard; DNA; 27 BP.
XX
AC AAZ09162;
XX
DT 18-OCT-1999 (first entry)
XX
DE Human tumour necrosis factor binding protein probe.
XX
KW Tumour necrosis factor binding protein; TNF; insoluble protein; agonist;
KW anti-inflammatory; antimalarial; treatment; septic shock; inflammation;
KW autoimmune glomerulonephritis; cerebral malaria; immune response;
KW antagonist; diagnosis; ss.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN EP939121-A2.
XX
PD 01-SEP-1999.
XX
PF 31-AUG-1990; 90EP-0116707.
XX
PR 20-APR-1990; 90CH-0001347.
PR 12-SEP-1989; 89CH-0003319.
PR 08-MAR-1990; 90CH-0000746.
XX
PA (HOFF) HOFFMANN LA ROCHE & CO AG F.
XX
PI Brockhaus M, Dembic Z, Gentz R, Lesslauer W, Loetscher H;
PI Schlaeger E;

XX
DR WPI; 1999-480840/41.
XX
PT New insoluble proteins, and fragments, that bind to tumor necrosis
PT factor, used to treat e.g. septic shock or cerebral malaria
XX
PS Example 8; Page 12; 25pp; German.
XX
CC This invention describes novel homogeneous insoluble proteins (I),
CC their (in)soluble fragments (Ia) and their salts that can bind tumour
CC necrosis factor (TNF). The products of the invention have
CC anti-inflammatory and antimalarial activity. (I) and (Ia) are used (i)
CC to treat diseases in which TNF is involved (e.g. septic shock, autoimmune
CC glomerulonephritis, cerebral malaria, immune responses and inflammation),
CC (ii) to purify TNF, (iii) to identify TNF (ant)agonists and (iv) for
CC diagnostic determination of TNF in body fluids. Antibodies raised against
CC (I) are used for affinity purification of (I). This sequence represents
CC a probe used in the method of the invention.
XX
SQ Sequence 27 BP; 8 A; 3 C; 11 G; 5 T; 0 other;

Query Match 1.2%; Score 27; DB 20; Length 27;
Best Local Similarity 100.0%; Pred. No. 5e+03;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 364 agggagaagagagatagtgtgtgtccc 390
||||||||||||||||||||||||||||
Db 1 agggagaagagagatagtgtgtgtccc 27

RESULT 2
AAH48867
ID AAH48867 standard; DNA; 27 BP.
XX
AC AAH48867;
XX
DT 12-NOV-2001 (first entry)
XX
DE Human 55 kD TNFBP probe DNA.
XX
KW TNF; tumor necrosis factor binding protein; TNFBP; treatment;
KW insoluble protein; antiinflammatory; immunosuppressive; antibacterial;
KW antiprotozoal; treatment; meningococcal sepsis; cerebral malaria;
KW autoimmune glomerulonephritis; probe; ss.
XX
OS Homo sapiens.
XX
PN EP1132471-A2.
XX
PD 12-SEP-2001.
XX
PF 31-AUG-1990; 2001EP-0108117.
XX
PR 12-SEP-1989; 89CH-0003319.
PR 08-MAR-1990; 90CH-0000746.
PR 20-APR-1990; 90CH-0001347.
PR 31-AUG-1990; 90EP-0116707.
PR 31-AUG-1990; 99EP-0100703.
XX
PA (HOFF) HOFFMANN LA ROCHE & CO AG F.
XX
PI Brockhaus M, Dembic Z, Gentz R, Lesslauer W, Loetscher H;
PI Schlaeger E;
XX
DR WPI; 2001-559312/63.
XX
PT New homogeneous, insoluble proteins that bind tumor necrosis factor
PT (TNF), useful for treating TNF-mediated disorders, e.g. inflammation
XX
PS Example 8; Page 13; 26pp; German.
XX
CC This invention describes novel insoluble proteins (I), also their
CC (in)soluble fragments and pharmaceutically acceptable salts, able to bind
CC tumor necrosis factor (TNF) and in homogeneous form. The products of the
CC invention have antiinflammatory, immunosuppressive, antibacterial,
CC antiprotozoal activity. (I), and related recombinant proteins, are used
CC to treat diseases mediated by TNF, e.g. shock in cases of meningococcal
CC sepsis; development of autoimmune glomerulonephritis and cerebral
CC malaria. Also (I), or antibodies specific for them, are used for
CC diagnostic determination of TNF in body fluids, for affinity purification
CC of TNF and for identifying (ant)agonists of TNF. This sequence represents
CC a probe used in the detection of the human 55 kD TNFBP described
CC in the method of the invention.
XX
SQ Sequence 27 BP; 8 A; 3 C; 11 G; 5 T; 0 other;

Query Match 1.2%; Score 27; DB 22; Length 27;
Best Local Similarity 100.0%; Pred. No. 5e+03;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 364 agggagaagagagatagtgtgtgtccc 390
||||||||||||||||||||||||||||
Db 1 agggagaagagagatagtgtgtgtccc 27

RESULT 3
AAX58185
ID AAX58185 standard; DNA; 25 BP.
XX
AC AAX58185;
XX
DT 21-JUL-1999 (first entry)
XX
DE Primer for CadC-fusion protein construction.
XX
KW CadC; fusion protein; erythropoietin receptor dimerisation domain;
KW protein-protein interaction; periplasmic domain; transmembrane domain;
KW CadC transcriptional regulatory domain; receptor interaction;
KW ligand identification; orphan receptor; ss.
XX
OS Synthetic.
XX
PN WO9923116-A1.
XX
PD 14-MAY-1999.
XX
PF 03-NOV-1998; 98WO-US23307.
XX
PR 09-SEP-1998; 98US-0149922.
PR 03-NOV-1997; 97US-0064058.
XX
PA (SMAL-) SMALL MOLECULE THERAPEUTICS INC.
XX
PI Hsing W, Menzel R, Taggart PA;
XX
DR WPI; 1999-313305/26.
XX
PT New CadC-fusion polypeptide nucleic acid constructs
XX
PS Example; Page 83; 123pp; English.
XX
CC This sequence represents a PCR primer used in the construction of a
CC CadC-fusion polypeptide.
CC The invention relates to CadC-fusion polypeptide nucleic acid constructs,
CC which are used to transform cells to produce systems for identifying
CC compounds which modulate interactions between protein sequences. The
CC CadC-fusion polypeptides comprise a periplasmic domain, a transmembrane
CC domain and a CadC transcriptional regulatory domain. Cells transformed
CC with nucleic acid encoding the fusion proteins and a cadBA reporter
CC construct can be used for identifying compounds which modulate a specific
CC protein-protein interaction such as modulation of interactions between
CC protein sequences involved in receptor interactions, e.g. dimerisation.
CC Such methods can be used for identifying ligands for orphan receptors.
CC The system is extremely sensitive in that background is low and the

```
CC   magnitude of signal background is quite robust, such that even minor
CC   modulations in protein-protein interactions are readily detectable.
XX
SQ   Sequence 25 BP; 2 A; 9 C; 7 G; 7 T; 0 other;


  Query Match           1.2%;  Score 25;  DB 20;  Length 25;
  Best Local Similarity  100.0%;  Pred. No. 1.4e+04;
  Matches   25;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     248 tgtctggcatgggcctctccaccgt 272
           |||||||||||||||||||||||||
Db       1 tgtctggcatgggcctctccaccgt 25


RESULT
AAA95191/c
ID   AAA95191 standard; DNA; 25 BP.
XX
AC   AAA95191;
XX
DT   12-JAN-2001  (first entry)
XX
DE   Reverse primer used to amplify exon 6 of TNFR1 gene.
XX
KW   TNFR1; tumour necrosis factor receptor; polymorphism; human;
KW   tumour; cancer; apoptosis; bacterial infection; primer; ss.
XX
OS   Homo sapiens.
XX
PN   WO200050436-A1.
XX
PD   31-AUG-2000.
XX
PF   23-FEB-2000; 2000WO-US04606.
XX
PR   23-FEB-1999;   99US-0121314.
XX
PA   (GENA-) GENAISSANCE PHARM INC.
PA   (NAND/) NANDABALAN K.
PA   (SCHU/) SCHULZ V P.
PA   (STEP/) STEPHENS J C.
PA   (CHEW/) CHEW A.
XX
PI   Nandabalan K,  Schulz VP,  Stephens JC,  Chew A;
XX
DR   WPI; 2000-543909/49.
XX
PT   Polynucleotides comprising polymorphic variants of a reference sequence
PT   for tumour necrosis factor receptor 1 (TNFR1), useful for studying the
PT   biological function of TNFR1 and identifying drugs targeting the
PT   protein for treating disorders -
XX
PS   Example 1; Page 31; 79pp; English.
XX
CC   The present invention relates to polymorphic variants of the tumour
CC   necrosis factor receptor 1 (TNFR1) gene. The sequence of the gene is
CC   given in AAA95102, AAA95103 and AAA95104. The polymorphisms were
CC   identified by amplifying and sequencing regions of the gene. Twelve
CC   polymorphic loci were discovered. Of these twelve polymorphisms, four can
CC   cause a change in the TNFR1 protein. The present sequence is a primer
CC   used to amplify part of the TNFR1 gene. The TNFR1 polymorphisms may be
CC   useful for studying the biological function of TNFR1 as well as for
CC   identifying drugs targeting the protein for treatment of disorders
CC   related to its abnormal expression or function such as tumours,
CC   apoptosis related disorders and bacterial infection.
XX
SQ   Sequence 25 BP; 5 A; 8 C; 4 G; 8 T; 0 other;


  Query Match           1.2%;  Score 25;  DB 21;  Length 25;
  Best Local Similarity  100.0%;  Pred. No. 1.4e+04;
  Matches   25;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     855 gaatgttaagggcactgaggactca 879
           |||||||||||||||||||||||||
Db      25 GAATGTTAAGGGCACTGAGGACTCA 1


RESULT   5
AAZ50185
ID   AAZ50185 standard; DNA; 30 BP.
XX
AC   AAZ50185;
XX
DT   04-MAY-2000  (first entry)
XX
DE   XbaI primer for D1-V84 and D1-L154 fragment amplification.
XX
KW   PCR primer; modulator; protein function; metabolic disorder; diabetes;
KW   tagged dominant negative element; TDNE; gene therapy; porphyria;
KW   proliferative disorder; endocrine disorder; obesity; phenylketonuria;
KW   arrhythmia; tumour necrosis factor alpha; TNF alpha; human ss.
XX
OS   Homo sapiens.
XX
PN   WO200005417-A1.
XX
PD   03-FEB-2000.
XX
PF   23-JUL-1999;   99WO-US16749.
XX
PR   23-JUL-1998;   98US-0093855.
XX
PA   (SMAL-) SMALL MOLECULE THERAPEUTICS INC.
XX
PI   Menzel R,  Khazak V;
XX
DR   WPI; 2000-182729/16.
XX
PT   Identification modulatory elements of functional protein interaction
PT   for use in determining biological activity of the protein and for
PT   treating diseases -
XX
PS   Example 6; Page 78; 104pp; English.
XX
CC   The patent discloses methods for determination of protein function and
CC   identifying modulators. This involves use of tagged dominant negative
CC   element (TDNE) that interferes with the interaction between a target and
CC   a partner protein comprising expressing TDNE in a microbial cell,
CC   measuring reporter gene expression and comparing the level to a
CC   expression level obtained in the absence of TDNE. The TDNEs are used in
CC   gene therapy and in screening for modulators. This is used for treating
CC   metabolic, proliferative, or endocrine disorders like diabetes, obesity,
CC   porphyria, phenylketonuria and arrhythmias. The present sequence is
CC   XbaI primer, used for amplification of tumour necrosis factor (TNF)
CC   alphaR extracellular domain (ECD) fragments, D1-V84 and D1-L154. The
CC   amplified products can be used to produce MalE fusion plasmids.
XX
SQ   Sequence 30 BP; 8 A; 6 C; 9 G; 7 T; 0 other;


  Query Match           1.2%;  Score 25;  DB 21;  Length 30;
  Best Local Similarity  100.0%;  Pred. No. 1.5e+04;
  Matches   25;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     373 agagatagtgtgtgtccccaaggaa 397
           |||||||||||||||||||||||||
Db       6 agagatagtgtgtgtccccaaggaa 30


RESULT   6
AAQ11261/c
ID   AAQ11261 standard; DNA; 24 BP.
XX
AC   AAQ11261;
```

XX
DT 13-MAY-1991 (first entry)
XX
DE Probe for clone encoding 30kD TNF inhibitor.
XX
KW Tumour necrosis factor; inhibitor; ss.
XX
OS Synthetic.
XX
PN AU9058976-A.
XX
PD 24-JAN-1991.
XX
PF 16-JUL-1990; 90AU-0058976.
XX
PR 07-FEB-1990; 90US-0479661.
PR 18-JUL-1989; 89US-0381080.
PR 11-DEC-1989; 89US-0450329.
XX
PA (SYNE-) SYNERGEN INC.
XX
DR WPI; 1991-073847/11.
XX
PT Tumour necrosis factor inhibitor - for suppression of TNF-alpha
PT and -beta, useful as therapeutic agent.
XX
PS Disclosure; Page 53; 142pp; English.
XX
CC The sequence corresponds to bases 671-694 of AAQ10878. It was used to
CC isolate clones contg. the sequence for the 30 kD TNF inhibitor from
CC a human genomic library. The whole gene can be inserted into
CC expression vectors for prepn. of TNF inhibitor for use in the
CC treatment of inflammatory and degenerative diseases.
CC See also AAQ11256-Q11267.
XX
SQ Sequence 24 BP; 4 A; 8 C; 7 G; 5 T; 0 other;

Query Match 1.1%; Score 24; DB 12; Length 24;
Best Local Similarity 100.0%; Pred. No. 2.3e+04;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 460 tacaatgactgtccaggcccgggg 483
||||||||||||||||||||||||
Db 24 TACAATGACTGTCCAGGCCCGGGG 1

RESULT 7
AAZ48478
ID AAZ48478 standard; DNA; 24 BP.
XX
AC AAZ48478;
XX
DT 31-MAR-2000 (first entry)
XX
DE Human TNFR1 DNA hybridising probe.
XX
KW Tumour necrosis factor receptor type 1; TNFR1; antisense; infection;
KW inflammation; tumour formation; TNFR1; anticancer; probe; ss.
XX
OS Homo sapiens.
XX
PN US6007995-A.
XX
PD 28-DEC-1999.
XX
PF 26-JUN-1998; 98US-0106038.
XX
PR 26-JUN-1998; 98US-0106038.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Baker BF, Cowsert LM;
XX
DR WPI; 2000-105333/09.
XX
PT Antisense inhibition of tumor necrosis factor type 1 expression for
PT diagnosis, treatment and prevention of disease, particularly tumors -
XX
PS Example 14; Column 28; 34pp; English.
XX
CC The invention provides antisense compounds targeted to human tumour
CC necrosis factor receptor type 1 (TNFR1) RNA. These antisense compounds
CC can be used in a method of inhibiting the expression of TNFR1 human cells
CC or tissues. The antisense compounds specifically hybridize with one or
CC more nucleic acids encoding TNFR1 modulating the function of nucleic
CC acid molecules encoding TNFR1, ultimately modulating the amount of TNFR1
CC produced. The antisense compounds and method are useful as research
CC reagents and diagnostics, and in the treatment and prophylaxis of
CC infection, inflammation or tumour formation. The present sequence
CC represents a probe hybridising to the human TNFR1 DNA.
XX
SQ Sequence 24 BP; 7 A; 7 C; 6 G; 4 T; 0 other;

Query Match 1.1%; Score 24; DB 21; Length 24;
Best Local Similarity 100.0%; Pred. No. 2.3e+04;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 554 tcagctgctccaaatgccgaaagg 577
||||||||||||||||||||||||
Db 1 tcagctgctccaaatgccgaaagg 24

RESULT 8
AAC83958/c
ID AAC83958 standard; DNA; 24 BP.
XX
AC AAC83958;
XX
DT 02-MAR-2001 (first entry)
XX
DE Human 30 kDa TNF inhibitor probe #6.
XX
KW TNF inhibitor; antiinflammatory; Tumour Necrosis Factor; interleukin;
KW IL-1; inflammatory disease; degenerative disease; human; probe; ss.
XX
OS Homo sapiens.
XX
PN US6143866-A.
XX
PD 07-NOV-2000.
XX
PF 19-JAN-1995; 95US-0375242.
XX
PR 19-JUL-1990; 90US-0555274.
PR 09-JUL-1993; 93US-0090366.
PR 18-JUL-1989; 89US-0381080.
PR 11-DEC-1989; 89US-0450329.
PR 07-FEB-1990; 90US-0479661.
XX
PA (AMGE-) AMGEN INC.
XX
PI Squires C, King MW, Hale KK, Brewer MT, Thompson RC;
PI Vanderslice RW, Vannice J, Kohno T;
XX
DR WPI; 2001-006443/01.
XX
PT Novel 30 kDa tumor necrosis factor inhibitor analog comprising a
PT non-native cysteine residue cross-linked with polyethylene glycol,
PT useful for treating inflammatory and degenerative diseases mediated by
PT TNF -
XX
PS Example 6; Column 28; 82pp; English.
XX
CC The present invention relates to Tumour Necrosis Factor (TNF) inhibitors

```
CC   (see AAB37676 and AAB37685), which have TNF inhibitory activity. The
CC   novel TNF inhibitors of the present invention are useful as therapeutic
CC   agents for inhibiting the activity of TNF and interleukin (IL-1), and
CC   for treating inflammatory and degenerative diseases mediated by TNF. The
CC   present sequence is a probe for the coding sequence for 30 kDa TNF
CC   inhibitor (AAC83945 and AAB37676). The 30 kDa TNF inhibitor can inhibit
CC   TNF alpha.
XX
SQ   Sequence 24 BP; 4 A; 8 C; 7 G; 5 T; 0 other;


  Query Match             1.1%;  Score 24;  DB 22;  Length 24;
  Best Local Similarity   100.0%;  Pred. No. 2.3e+04;
  Matches   24;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     460 tacaatgactgtccaggcccgggg 483
           ||||||||||||||||||||||||
Db      24 TACAATGACTGTCCAGGCCCGGGG 1


RESULT   9
AAT93813
ID   AAT93813 standard; DNA; 28 BP.
XX
AC   AAT93813;
XX
DT   24-FEB-1998  (first entry)
XX
DE   Antitumoural phosphodiester oligonucleotide 3 with cytotoxic activity.
XX
KW   Phosphodiester; selective binding; cell viability; growth;
KW   tumoural cell line; cytotoxic activity; tumour cell; lymphoma;
KW   lymphoblastic tumour; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base   1..28
FT                   /*tag= a
FT                   /note= "phosphodiester oligonucleotide"
XX
PN   WO9720924-A1.
XX
PD   12-JUN-1997.
XX
PF   04-DEC-1996;   96WO-EP05388.
XX
PR   04-DEC-1995;   95IT-0MI2539.
XX
PA   (SAIC-) SAICOM SRL.
XX
PI   Quadrifoglio F,  Scaggiante B;
XX
DR   WPI; 1997-319771/29.
XX
PT   New phospho:di:esteric oligo:nucleotide(s) - which exert a specific
PT   and selective cytotoxic effect on tumour cells, for treating both
PT   solid and liquid tumours
XX
PS   Claim 10; Page 5; 38pp; English.
XX
CC   Novel phosphodiesteric oligonucleotides AAT93811-27 are based on the
CC   generic formula, in the 3'-5' or 5'-3' direction:
CC   (GaTa')a''-(GbTb')b''-(GcTc')c''-(GdTd')d''-(GeTe')e''-(GfTf')f''-
CC   (G-gTg')g''-N', where:
CC   N and N' = T or G, equal or different from each other;
CC   x = 0-8, equal or different from each other;
CC   a, b, c, d, e, f, and g = 0-10, equal or different from each other;
CC   a', b', c', d', e', f', and g' = 0-30, equal or different from each
CC   other;
CC   a'', b'', c'', d'', e'', f'', and g'' = 1-16, equal or different from
CC   each other;
CC   The oligonucleotides are believed to selectively bind and sequester
CC   some proteins which are essential to the viability and growth of
CC   tumoural cell line. They have specific and selective cytotoxic activity
CC   against tumour cells, and can be used for treating tumours of the liquid
CC   type, in particular of lymphoblastic origin, and of solid type, in
CC   particular lymphomas. The present phosphodiester oligonucleotide, at a
CC   concentration of 15 micromolar, reduced growth of CCRF-CEM tumoural
CC   cells by 78%, which is detectable 48 hours after administration.
XX
SQ   Sequence 28 BP; 0 A; 0 C; 6 G; 22 T; 0 other;


  Query Match             1.1%;  Score 24;  DB 18;  Length 28;
  Best Local Similarity   100.0%;  Pred. No. 2.5e+04;
  Matches   24;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    1976 ttttgttttgttttgttttgtttt 1999
           ||||||||||||||||||||||||
Db       3 ttttgttttgttttgttttgtttt 26


RESULT  10
AAZ09169/c
ID   AAZ09169 standard; DNA; 29 BP.
XX
AC   AAZ09169;
XX
DT   18-OCT-1999  (first entry)
XX
DE   Human 55kDa tumour necrosis factor binding protein PCR primer 2.
XX
KW   Tumour necrosis factor binding protein; TNF; insoluble protein; agonist;
KW   anti-inflammatory; antimalarial; treatment; septic shock; inflammation;
KW   autoimmune glomerulonephritis; cerebral malaria; immune response;
KW   antagonist; diagnosis; PCR primer; ss.
XX
OS   Synthetic.
OS   Homo sapiens.
XX
PN   EP939121-A2.
XX
PD   01-SEP-1999.
XX
PF   31-AUG-1990;   90EP-0116707.
XX
PR   20-APR-1990;   90CH-0001347.
PR   12-SEP-1989;   89CH-0003319.
PR   08-MAR-1990;   90CH-0000746.
XX
PA   (HOFF ) HOFFMANN LA ROCHE & CO AG F.
XX
PI   Brockhaus M,  Dembic Z,  Gentz R,  Lesslauer W,  Loetscher H;
PI   Schlaeger E;
XX
DR   WPI; 1999-480840/41.
XX
PT   New insoluble proteins, and fragments, that bind to tumor necrosis
PT   factor, used to treat e.g. septic shock or cerebral malaria
XX
PS   Example 11; Page 16; 25pp; German.
XX
CC   This invention describes novel homogeneous insoluble proteins (I),
CC   their (in)soluble fragments (Ia) and their salts that can bind tumour
CC   necrosis factor (TNF). The products of the invention have
CC   anti-inflammatory and antimalarial activity. (I) and (Ia) are used (i)
CC   to treat diseases in which TNF is involved (e.g. septic shock, autoimmune
CC   glomerulonephritis, cerebral malaria, immune responses and inflammation),
CC   (ii) to purify TNF, (iii) to identify TNF (ant)agonists and (iv) for
CC   diagnostic determination of TNF in body fluids. Antibodies raised against
CC   (I) are used for affinity purification of (I). This sequence represents
CC   a PCR primer used in the amplification of the TNF binding protein of the
CC   invention.
XX
SQ   Sequence 29 BP; 5 A; 7 C; 9 G; 8 T; 0 other;
```

```
  Query Match             1.1%;  Score 23.8;  DB 20;  Length 29;
  Best Local Similarity   92.6%;  Pred. No. 2.8e+04;
  Matches   25;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy    869 ctgaggactcaggcaccacagtgctgt 895
          ||||||||||||||||||| ||| |
Db     29 CTGAGGACTCAGGCACCACAGAGCTCT 3


RESULT  11
AAH48858/c
ID   AAH48858 standard; DNA; 29 BP.
XX
AC   AAH48858;
XX
DT   12-NOV-2001  (first entry)
XX
DE   Human 55 kD TNFBP extracellular fragment PCR primer 2.
XX
KW   TNF; tumor necrosis factor binding protein; TNFBP; treatment;
KW   insoluble protein; antiinflammatory; immunosuppressive; antibacterial;
KW   antiprotozoal; treatment; meningococcal sepsis; cerebral malaria;
KW   autoimmune glomerulonephritis; PCR primer; ss.
XX
OS   Homo sapiens.
XX
PN   EP1132471-A2.
XX
PD   12-SEP-2001.
XX
PF   31-AUG-1990; 2001EP-0108117.
XX
PR   12-SEP-1989;   89CH-0003319.
PR   08-MAR-1990;   90CH-0000746.
PR   20-APR-1990;   90CH-0001347.
PR   31-AUG-1990;   90EP-0116707.
PR   31-AUG-1990;   99EP-0100703.
XX
PA   (HOFF ) HOFFMANN LA ROCHE & CO AG F.
XX
PI   Brockhaus M,  Dembic Z,  Gentz R,  Lesslauer W,  Loetscher H;
PI   Schlaeger E;
XX
DR   WPI; 2001-559312/63.
XX
PT   New homogeneous, insoluble proteins that bind tumor necrosis factor
PT   (TNF), useful for treating TNF-mediated disorders, e.g. inflammation -
XX
PS   Example 11; Page 16; 26pp; German.
XX
CC   This invention describes novel insoluble proteins (I), also their
CC   (in)soluble fragments and pharmaceutically acceptable salts, able to bind
CC   tumor necrosis factor (TNF) and in homogeneous form. The products of the
CC   invention have antiinflammatory, immunosuppressive, antibacterial,
CC   antiprotozoal activity. (I), and related recombinant proteins, are used
CC   to treat diseases mediated by TNF, e.g. shock in cases of meningococcal
CC   sepsis; development of autoimmune glomerulonephritis and cerebral
CC   malaria. Also (I), or antibodies specific for them, are used for
CC   diagnostic determination of TNF in body fluids, for affinity purification
CC   of TNF and for identifying (ant)agonists of TNF. This sequence represents
CC   a PCR primer used in the amplification of the human 55 kD TNFBP described
CC   in the method of the invention.
XX
SQ   Sequence 29 BP; 5 A; 7 C; 9 G; 8 T; 0 other;


  Query Match             1.1%;  Score 23.8;  DB 22;  Length 29;
  Best Local Similarity   92.6%;  Pred. No. 2.8e+04;
  Matches   25;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy    869 ctgaggactcaggcaccacagtgctgt 895
          ||||||||||||||||||| ||| |
Db     29 CTGAGGACTCAGGCACCACAGAGCTCT 3


RESULT  12
AAQ11256/c
ID   AAQ11256 standard; DNA; 23 BP.
XX
AC   AAQ11256;
XX
DT   13-MAY-1991  (first entry)
XX
DE   Probe for clone encoding 30kD TNF inhibitor.
XX
KW   Tumour necrosis factor; inhibitor; ss.
XX
OS   Synthetic.
XX
PN   AU[illegible]8976-A.
XX
PD   24-JAN-1991.
XX
PF   16-JUL-1990;   90AU-0058976.
XX
PR   07-FEB-1990;   90US-0479661.
PR   18-JUL-1989;   89US-0381080.
PR   11-DEC-1989;   89US-0450329.
XX
PA   (SYNE-) SYNERGEN INC.
XX
DR   WPI; 1991-073847/11.
XX
PT   Tumour necrosis factor inhibitor - for suppression of TNF-alpha
PT   and -beta, useful as therapeutic agent.
XX
PS   Disclosure; Page 49; 142pp; English.
XX
CC   The sequence corresponds to bases 410-433 of AAQ10878. It was used to
CC   isolate clones contg. the sequence for the 30 kD TNF inhibitor from
CC   a human genomic library.   The whole gene can be inserted into
CC   expression vectors for prepn. of TNF inhibitor for use in the
CC   treatment of inflammatory and degenerative diseases.
CC   See also AAQ11257-Q11267.
XX
SQ   Sequence 23 BP; 6 A; 4 C; 6 G; 7 T; 0 other;


  Query Match             1.1%;  Score 23;  DB 12;  Length 23;
  Best Local Similarity   100.0%;  Pred. No. 3.9e+04;
  Matches   23;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    424 atttgctgtaccaagtgccacaa 446
          |||||||||||||||||||||||
Db     23 ATTTGCTGTACCAAGTGCCACAA 1


RESULT  13
AAQ69116/c
ID   AAQ69116 standard; DNA; 23 BP.
XX
AC   AAQ69116;
XX
DT   23-FEB-1995  (first entry)
XX
DE   p55 TNF-R gene 5' flanking sequence probe.
XX
KW   5' flanking region; p55 tumour necrosis factor receptor; TNF-R;
KW   promoter; CAT reporter gene; human; HeLa cell; mouse; A9 cell;
KW   transcription start point; S1 nuclease digestion; U 937 cell; probe;
KW   multiple start sites of transcription; house-keeping gene;
KW   hypoxanthine phosphoribosyltransferase; EGF receptor; NGF receptor;
KW   p55 IL-1 receptor; TATA box; CCAAT motif; methylation; ss.
XX
```

OS Synthetic.
XX
PN EP606869-A.
XX
PD 20-JUL-1994.
XX
PF 10-JAN-1994; 94EP-0100243.
XX
PR 10-JAN-1993; 93IL-0104355.
XX
PA (YEDA) YEDA RES & DEV CO LTD.
XX
PI Kemper O, Wallach D;
XX
DR WPI; 1994-226810/28.
XX
PT Promoter sequence of the p55 TNF receptor - is used to diagnose
PT mutations in the promoter region which contribute to pathology of
PT diseases
XX
PS Disclosure; Column 3; 14pp; English.
XX
CC This sequence represents a probe for the isolation and sequencing of
CC the 5' flanking region of the p55 tumour necrosis factor receptor
CC (TNF-R) gene. This isolated fragment was found to have promoter
CC activity, shown by its ability to drive expression of the CAT reporter
CC gene in both human HeLa cells and mouse A9 cells. Deletion constructs
CC of this clone showed that promoter activity was confined to a 150 bp
CC BglII-EcoRI fragment which included most of the transcription start
CC point. Further analysis showed that a minimal promoter of 70 bp still
CC exhibited activity. S1 nuclease digestion analysis of the RNA of the
CC HeLa and U 937 cells with DNA probes indicated multiple start sites of
CC transcription. It was found that the promoter sequence resembles
CC promoters of house-keeping genes, eg. hypoxanthine phosphoribosyl-
CC transferase, EGF receptor, NGF receptor or the p55 IL-1 receptor. It
CC is devoid of a TATA box and of a CCAAT motif and is relatively rich in
CC G/C in its 3' end. There is an even higher content of G/C residues in
CC the proximally located, 5' end of the first intron. This region is also
CC rich in the dinucleotide couple CpG, which may allow for differentiation-
CC related changes in the promoter activity as a function of the extent of
CC methylation of these nucleotides.
XX
SQ Sequence 23 BP; 5 A; 2 C; 10 G; 6 T; 0 other;

```
  Query Match             1.1%;  Score 23;  DB 15;  Length 23;
  Best Local Similarity   100.0%;  Pred. No. 3.9e+04;
  Matches   23;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     122 agtctcaaccctcaactgtcacc 144
           |||||||||||||||||||||||
Db      23 AGTCTCAACCCTCAACTGTCACC 1
```

RESULT 14
AAQ69119/c
ID AAQ69119 standard; DNA; 23 BP.
XX
AC AAQ69119;
XX
DT 23-FEB-1995 (first entry)
XX
DE p55 TNF-R gene 5' flanking sequence primer 3.
XX
KW 5' flanking region; p55 tumour necrosis factor receptor; TNF-R;
KW promoter; CAT reporter gene; human; HeLa cell; mouse; A9 cell;
KW transcription start point; S1 nuclease digestion; U 937 cell; probe;
KW multiple start sites of transcription; house-keeping gene;
KW hypoxanthine phosphoribosyltransferase; EGF receptor; NGF receptor;
KW p55 IL-1 receptor; TATA box; CCAAT motif; methylation; ss.
XX
OS Synthetic.
XX
PN EP606869-A.
XX
PD 20-JUL-1994.
XX
PF 10-JAN-1994; 94EP-0100243.
XX
PR 10-JAN-1993; 93IL-0104355.
XX
PA (YEDA) YEDA RES & DEV CO LTD.
XX
PI Kemper O, Wallach D;
XX
DR WPI; 1994-226810/28.
XX
PT Promoter sequence of the p55 TNF receptor - is used to diagnose
PT mutations in the promoter region which contribute to pathology of
PT diseases
XX
PS Example 3; Column 8; 14pp; English.
XX
CC This sequence is a primer which was used in the determination of the
CC multiple transcription start sites of the 5' flanking region of the p55
CC tumour necrosis factor receptor (TNF-R) gene. This isolated fragment
CC was found to have promoter activity, shown by its ability to drive
CC expression of the CAT reporter gene in both human HeLa cells and mouse
CC A9 cells. Deletion constructs of this clone showed that promoter
CC activity was confined to a 150 bp BglII-EcoRI fragment which included
CC most of the transcription start point. Further analysis showed that a
CC minimal promoter of 70 bp still exhibited activity. S1 nuclease
CC digestion analysis of the RNA of the HeLa and U 937 cells with DNA
CC probes indicated multiple start sites of transcription. It was found
CC that the promoter sequence resembles promoters of house-keeping genes,
CC eg. hypoxanthine phosphoribosyl-transferase, EGF receptor, NGF receptor
CC or the p55 IL-1 receptor. It is devoid of a TATA box and of a CCAAT
CC motif and is relatively rich in G/C in its 3' end. There is an even
CC higher content of G/C residues in the proximally located, 5' end of the
CC first intron. This region is also rich in the dinucleotide couple CpG,
CC which may allow for differentiation-related changes in the promoter
CC activity as a function of the extent of methylation of these nucleotides.
XX
SQ Sequence 23 BP; 5 A; 2 C; 10 G; 6 T; 0 other;

```
  Query Match             1.1%;  Score 23;  DB 15;  Length 23;
  Best Local Similarity   100.0%;  Pred. No. 3.9e+04;
  Matches   23;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     122 agtctcaaccctcaactgtcacc 144
           |||||||||||||||||||||||
Db      23 AGTCTCAACCCTCAACTGTCACC 1
```

RESULT 15
AAZ48476
ID AAZ48476 standard; DNA; 23 BP.
XX
AC AAZ48476;
XX
DT 31-MAR-2000 (first entry)
XX
DE Human TNFR1 DNA amplifying forward primer.
XX
KW Tumour necrosis factor receptor type 1; TNFR1; antisense; infection;
KW inflammation; tumour formation; TNFR1; anticancer; PCR primer; ss.
XX
OS Homo sapiens.
XX
PN US6007995-A.
XX
PD 28-DEC-1999.
XX
PF 26-JUN-1998; 98US-0106038.
XX

PR 26-JUN-1998; 98US-0106038.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Baker BF, Cowsert LM;
XX
DR WPI; 2000-105333/09.
XX
PT Antisense inhibition of tumor necrosis factor type 1 expression for
PT diagnosis, treatment and prevention of disease, particularly tumors -
XX
PS Example 14; Column 28; 34pp; English.
XX
CC The invention provides antisense compounds targeted to human tumour
CC necrosis factor receptor type 1 (TNFR1) RNA. These antisense compounds
CC can be used in a method of inhibiting the expression of TNFR1 human cells
CC or tissues. The antisense compounds specifically hybridize with one or
CC more nucleic acids encoding TNFR1 modulating the function of nucleic
CC acid molecules encoding TNFR1, ultimately modulating the amount of TNFR1
CC produced. The antisense compounds and method are useful as research
CC reagents and diagnostics, and in the treatment and prophylaxis of
CC infection, inflammation or tumour formation. The present sequence
CC represents a primer for amplifying the human TNFR1 DNA.
XX
SQ Sequence 23 BP; 9 A; 8 C; 3 G; 3 T; 0 other;

Query Match 1.1%; Score 23; DB 21; Length 23;
Best Local Similarity 100.0%; Pred. No. 3.9e+04;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 526 gcttcagaaaaccacctcagaca 548
||||||||||||||||||||||||
Db 1 gcttcagaaaaccacctcagaca 23

Search completed: September 19, 2002, 04:11:46
Job time: 10401 sec